The Association for
Mass Spectrometry:
Applications to the Clinical Lab

MSACL 2016 US
The 8th Annual International Conference of
The Association for
Mass Spectrometry:
Applications to the Clinical Lab
Palm Springs, CA
February 21 - 25, 2016
Renaissance Hotel & Palm Springs Convention Center

The Association is a non-membership, non-profit 501(c)(3) tax-exempt California Corporation with the mission of furthering education in the field of mass spectrometry.

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Sponsorship & Travel Grant Support

**Platinum**
- $18,000

**Gold**
- $12,000

**Silver**
- $6,000

**Bronze**
- $3,000

**Travel Grant Support**
- $15,000
- $10,000
- $6,000
- $2,000
# Scientific Committee

**Chair**: David Herold, MD, PhD  
*University of California, San Diego  
VA Medical Center, San Diego*

### Endocrinology

<table>
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<tr>
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<th>Institution</th>
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<tbody>
<tr>
<td>Dan Holmes, MD (Lead)</td>
<td><em>St. Paul’s Hospital</em></td>
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<tr>
<td>Michael Chen, MD</td>
<td><em>McGill University</em></td>
</tr>
<tr>
<td>Brian Rappold</td>
<td><em>Essential Testing</em></td>
</tr>
<tr>
<td>Ravinder Singh, PhD</td>
<td><em>Mayo Clinic</em></td>
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### Metabolomics

<table>
<thead>
<tr>
<th>Name</th>
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<tbody>
<tr>
<td>Gary Patti PhD (Lead)</td>
<td><em>Washington University</em></td>
</tr>
<tr>
<td>Mohit Jain MD, PhD</td>
<td><em>University of California, San Diego</em></td>
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### Microbiology

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<tr>
<td>Susan Butler-Wu PhD</td>
<td><em>University of Southern California</em></td>
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<tr>
<td>Pieter Dorrestein, PhD</td>
<td><em>University of California, San Diego</em></td>
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<tr>
<td>Carey-Ann Burnham PhD</td>
<td><em>Washington University</em></td>
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<tr>
<td>Vanessa Phelan PhD</td>
<td><em>University of California, San Diego</em></td>
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<tr>
<td>Nathan Ledeboer, PhD</td>
<td><em>Medical College of Wisconsin</em></td>
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### Proteomics

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<tr>
<th>Name</th>
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<tbody>
<tr>
<td>Cory Bystrom, PhD (Lead)</td>
<td><em>Cleveland Heart Lab</em></td>
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<tr>
<td>Leigh Anderson, PhD</td>
<td><em>SISCAPA Assay Technologies</em></td>
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<td>Rob Fitzgerald, PhD (Lead)</td>
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<tr>
<td>University of California, San Diego</td>
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<tr>
<td>Judy Stone, PhD</td>
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<tr>
<td>University of California, San Diego</td>
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<tr>
<td>Julianne Botelho, PhD (Lead)</td>
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<td>CDC</td>
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<td>Victoria Zhang, PhD</td>
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<tr>
<td>University of Rochester</td>
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<td>Hubert Vesper, PhD</td>
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<td>CDC</td>
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<tr>
<td>Livia Eberlin, PhD (Lead)</td>
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<tr>
<td>University of Texas at Austin</td>
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<tr>
<td>Jeff Spragins, PhD</td>
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<tr>
<td>Vanderbilt University</td>
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<tr>
<td>Ron Heeren, Prof. Dr.</td>
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<tr>
<td>Maastricht University</td>
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<th>Toxicology / TDM / Pain</th>
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<tr>
<td>Kara Lynch PhD (Lead)</td>
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<tr>
<td>University of California, San Francisco</td>
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<tr>
<td>Jason Sawyer</td>
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<tr>
<td>ARUP</td>
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<tr>
<td>Jennifer Colby, PhD</td>
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<tr>
<td>Vanderbilt University</td>
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General Information

Continuing Education Credits
Continuing Education credits will be available on the MSACL website for the short courses and the Scientific Sessions through ACCENT by AACC. Go to: msacl.org > CE Credits > ACCENT > MSACL 2016 US

Conference Badges
Your badge constitutes your admission pass to the Conference, receptions and the Exhibit Hall. YOU ARE REQUIRED TO DISPLAY YOUR BADGE PROMINENTLY while attending the conference and at all associated functions. If you do not have your badge you will be escorted to the registration desk to get one, or off the premises. If you have an EXHIBITS ONLY badge YOU ARE NOT PERMITTED IN THE SCIENTIFIC SESSIONS, except the Plenary. If you are identified to be flouting this detail, your registration will be revoked without refund.

Yoga
Yoga will be held every day at 6:00 – 7:00 AM in San Jacinto in the Renaissance Hotel. MSACL will be providing a limited number of yoga mats and other accoutrements.

Smoking
Smoking is prohibited within the conference facility and outside within 50 ft of the building.

Tape Recording/Video Recording Policy
Please observe the MSACL policy which prohibits operation of tape recorders, video recorders, cameras, or camera phones, except for official association equipment, at all conference sessions, in the Exhibit Hall, and during the plenary sessions

Throughout Conferences MSACL will be videotaping and taking photographs to be used for promotional or educational purposes by MSACL. If you do not wish to appear on camera, please notify the videographer or photographer and your request will be honored.
Presenter Info and Guidelines

Podium Presentations

Location: Mojave Learning Center, Catalina, Madera, Pasadena, Sierra, SmokeTree A-E

- If an individual is unable to present or does not show, the presentation time slot will be left open. **It will not be filled by the next speaker.** The next speaker will begin presenting at his/her scheduled time.
  - **Back-Up Presenters:** If a presenter does not show a back-up presenter may be called to fill in the open spot. **Session Chairs, please contact registration immediately on determining that a speaker may not show so that efforts may be put in place to locate a back-up speaker.**
- Speakers: Please make an effort to repeat any questions from the audience before answering.
- Podium presentations are ~15 minutes with ~5 minutes for Q&A.
- PC Laptops running Windows 7 & Office 2007 and 365 will be provided.
- Presenters should check-in 15-30 minutes prior to their Session (NOT their talk) with either the Session Chair or AV Support on-hand to upload their presentation files to the primary presentation lap-top computer.
- Presenters must bring their presentations on thumb (USB) drives for placement on a single presentation computer from which all presenters will access their PowerPoint presentations.
- Laser pointers will be provided.

Poster Presentations

Location: Exhibit Hall

Poster sessions are held on Monday, Tuesday and Wednesday.

- Poster attendance is for 1 hour,
  - 7:00-8:00 PM (Mon)
  - 3:00-4:00 PM (Tue & Wed)
  - 5:00-6:00 PM (Tue & Wed)
- 7:00 PM Posters (Monday: All Posters)
  - Place on Poster Board before 4:00 PM
  - Attend from 7:00 - 8:00 PM
  - Remove between 8:30 – 9:00 PM
- 3:00 PM Posters (Even #: 2,4,6, etc)
  - Place on Poster Board before 8:00 AM
  - Attend from 3:00 - 4:00 PM
  - Remove between 7:00 – 7:30 PM
- 5:00 PM Posters (Odd #: 1,3,5,7 etc)
  - Place on Poster Board before 8:00 AM
  - Attend from 5:00 - 6:00 PM
  - Remove between 7:00 - 7:30 PM
- Maximum Poster dimensions (for each presenter) are 3.5 feet wide x 3.5 feet high.
- Poster Boards are Fabric.
- Poster Pins WILL BE provided.

Sharing Your Poster OR Slides

You may upload your poster or slides (at anytime) as a PDF file via Manage Abstract. Once the PDF is uploaded, a link to download the poster / slides will appear next you your abstract in the online program.
Plenary Speaker Series

**MSACL 2016 US - Distinguished Contribution Awardee**

What We Can Learn from a Drop of Urine – Metabolomics at it’s Earliest: Discoveries of Bile Acid Synthesis Disorders, a New Category of Fatal Metabolic Liver Disease and Development of a Treatment

Kenneth Setchell
*Cincinnati Children’s Hospital Medical Center*

Tuesday @ 9:30 AM in the California Ballroom *includes Award Presentation*

This presentation will highlight how mass spectrometry was successfully applied to define new genetic defects in the cholesterol-bile acid biosynthetic pathway as a specific class of metabolic liver disease. Bile acid synthesis disorders due to single enzyme defects generally present in infancy or early childhood with a progressive cholestatic hepatitis that, unchecked, lead to cirrhosis, liver failure, and death. Prior to the seminal work of Setchell and colleagues in identifying 6 genetic diseases as discrete entities, and conceiving of an effective therapy, children with these autosomal recessive diseases either underwent liver transplantation, or more commonly, were given supportive care until they died of liver failure of unknown origin. To be described are the combined use an untargeted and targeted approach with FAB-MS, GC-MS and ESI-LC-MS/MS that led to the elucidation of the biochemical basis of these diseases, the development of an international screening program, and the evaluation of the therapeutic responses that served to ultimately gain regulatory approval from the FDA for a life-saving therapy based on oral administration of cholic acid. This application of mass spectrometry to clinical chemistry has been a game-changer that has led to a radical change in the evaluation and treatment of patients with idiopathic progressive familial intrahepatic cholestasis syndromes.

**Diagnosis - The Beauty and the Beast**

Mark Graber
*Society to Improve Diagnosis in Medicine*

Wednesday @ 9:15 AM in the California Ballroom

Diagnosis is perhaps the most complicated cognitive task humans face. Despite the many challenges involved, the correct diagnosis is established in the great majority of cases, thanks in very large part to advances in medical testing, such as mass spectrometry. At the same time, diagnostic errors are too common and cause enormous harm. The origins of diagnostic errors will be explored, providing insights that can improve not only diagnosis, but the decisions we make in our everyday lives and research enterprises.
Immunotherapy of Cancer and the Role of Mass Spectrometry; an Overview
Donald Hunt
University of Virginia

Wednesday @ 10:00 AM in the California Ballroom

This lecture will describe how the immune system works to keep us free of cancer most of the time and how cancer cells can eventually learn to escape the immune system. Also described will be a number of scientific breakthroughs that have occurred in the last 6 years that clearly suggest that the immune system can be re-educated and upregulated to cure even late stage cancer. Science magazine labeled cancer immunotherapy as the breakthrough event of the year in 2013 and tremendous progress has been made since then. James Allison won the 2015 Lasker Award in medicine for his work to reactivate the immune system to fight cancer. You know this is a hot area for mass spectrometry when the research groups of Aebersold, Heck, Mann and Carr all decide to establish and work on the Human Immuno-Peptidome Project (HIPP) at the HUPO 2015 meeting in Vancouver. This lecture will try to capture some of this excitement and also pinpoint some of the contributions that the Hunt group has made to the field over the past 23 yrs.

Mass Spectrometry in Clinical Science
R. Graham Cooks
Purdue University

Thursday @ 9:15 AM in the California Ballroom

This presentation attempts to elucidate the forces converging to create a major increase in the applications (and applicability) of mass spectrometry in the clinic. The forces include: i) ambient ionization methods for direct examination of biological samples, including tissue and whole biofluids, ii) miniature mass spectrometers capable of unit resolution and MS/MS, iii) ion transfer over long distances to the Mini MS, iv) quantitation out of complex mixtures by multiple reaction monitoring (MRM), and v) multivariate data analysis for confident assignment of complex spectral patterns to particular biological and disease states. Example applications include surgical margins, drug and microorganism (e.g. strep) detection.
Young Investigator Grantees

This year seventy-one (71) Young Investigator Travel Grants were provided. Young Investigator Travel Awards are awarded to support trainees (MD/residents/fellows and PhD - students / post-docs) and young faculty members (less than 4 years since appointment) who have submitted a qualified abstract. These awards include conference and short course registration, partial lodging and, in the case of exceptional abstracts, partial travel coverage.

James Alexander Imperial College, London
Mohammad Alyamani Cleveland State University
Elizabeth Axton Oregon State University
Emily Bliss University College London
Mark Bokhart North Carolina State University
James Bollinger University of Washington Medical Center
Lori Bourassa University of Washington Medical Center
Dimitri Brinet Gothenburg University
Simon Cameron Imperial College London
Jonas Ceponis Los Angeles Biomedical Institute at Harbor-UCLA
Dawn Chen Cedars-Sinai Medical Center
Christopher Chouinard University of Florida
Jennifer Colby Vanderbilt University
Lewis Couchman King’s College Hospital
Chris Cox University of Oklahoma and Harvard University
Alireza Dehghani University of Bonn
Mari DeMarco University of British Columbia, St Paul’s Hospital
Maria Luisa Doria Imperial College, London
Jorg Hanrieder University of Gothenburg
Sophie Hepburn Prince of Wales Hospital
Melissa Hoffman Moffitt Cancer Center/University of South Florida
Howard Horng University of California, San Francisco
Alan Jarmusch Purdue University
Carl Jenkinson Metabolism and Systems Research (IMSR)
Feng Jin Baylor College of Medicine
Brooke Katzman Mayo Clinic
Francyne Kubaski University of Delaware/ Nemours-Alfred I. duPont Children Hospital
Yin-Ming Kuo Fox Chase Cancer Center
Yungkang Lee Berkshire Healthcare Systems
Chi-Wei Lee Kaohsiung Medical University
Yongchao Li University of Illinois at Chicago
Hsuan-Chieh Liao University of Washington
Camille Lombard-Banek The George Washington University
Jianqing (Ben) Lu Prince of Wales Hospital
Mark Marzinke Johns Hopkins University School of Medicine
Imir Metushi UC San Diego Health
Wojciech Michno University of Gothenburg
John Mills Mayo Clinic
Milad Nazari North Carolina State University
Peter Nemes George Washington University
Talia Novos Prince of Wales Hospital, SEALS

Dana Ohana Leiden University Medical Centre
Mariola Ołkowicz Medical University of Gdansk
Vasanta Putluri Baylor College of Medicine
Koen Raedschelders Heart Institute, Cedars Sinai Medical Center
Anna Robson Heart of England NHS Foundation Trust
Merja Rossi Imperial College, London
Joseph Rudolf Massachusetts General Hospital
Andraz Smon University Children’s Hospital, University Medical Centre Ljubljana
Edward St. John Imperial College, London
Sylvania Stopka The George Washington University
Linda Switzaer Leiden University Medical Center
Stefani Thomas Johns Hopkins University
Shahid Ullah Karolinska Institute
Ryan Walsh University of Colorado, Denver (Anschutz Medical Campus)
Evelyn Wang University of Texas at Arlington
Li Wang BC Children’s hospital
Jikang Wu The Ohio State University
Yi Xiao Children’s Hospital Los Angeles
He Yang Univ. of California, San Francisco/SF General Hospital
Yifei Yang Yale University
Han-Yin Yang University of Washington
Melanie Yarbrough Washington University School of Medicine
Tyler Yin University of Louisville
Yanbao Yu J. Craig Venter Institute
Jialing Zhang University of Texas, Austin
Shenyen Zhang Cedars Sinai Medical Center
Junfang Zhao Cincinnati Children’s Hospital Medical Center
Yu Zi (Emma) Zheng St. Paul’s Hospital, University of British Columbia
Jiangjiang (Chris) Zhu Miami University
Irina Zolkina Pirogov Russian National Research Medical University
Lab Director Grantees

This year, thirty-two (32) Lab Director Awards were granted to individuals leading clinical labs. These individuals have had minimal exposure to mass spectrometry and are interested in gaining more understanding of its potential applications.

Lindsay Bazydlo University of Virginia
Jessica Boyd Calgary Laboratory Services/University of Calgary
David Carpentieri Phoenix Children’s Hospital
Alex Chin Calgary Laboratory Services/University of Calgary
Jessica Colon-Franco Medical College of Wisconsin
Melkon DomBourian Children’s Hospital Colorado/University of Colorado
Kelly Doyle Intermountain Healthcare
Sucharita Dutta EVMS
Guy Fink CIUSSS de l’Estrie-Centre Hospitalier Universitaire de Sherbrooke
Xiaowei Fu University of Southern California
Stewart Graham Beaumont Health
Dina Greene University of Washington
Paul Jannetto Mayo Clinic
Benjamin Jung BC Children’s Hospital, Children’s and Women’s Health Centre of British Columbia
Thomas Kampfrath Santa Clara Valley Medical Center
Brian Kelly University of Utah
Dailin Li Vancouver General Hospital
Sara Love Hennepin County Medical Center
M. Laura Parnas Sutter Health Shared Laboratory
Nagireddy Putluri Baylor College of Medicine
Anna Romanelli University of California, Davis Health System
Ramesh Saeedi University of British Columbia
Alec Saitman Providence Regional Laboratories
Edward Sass University of Alabama in Huntsville
Vivekananda Shetty Baylor College of Medicine
Lingli Tang the Second Xiangya Hospital, Central South University
Margret Thorsteinsdottir University of Iceland
Antonius van Herwaarden Radboud University Medical Center
Faye Vicente Ann & Robert H. Lurie Children’s Hospital of Chicago
Rao Weiqiao BGI-Research
Kevin Xiao University of Pittsburgh
Xin Yi Houston Methodist Hospital
Trainee Grantees

This year, forty-three (43) Trainee Awards were granted to individuals training to lead clinical labs. These individuals have had minimal exposure to mass spectrometry and are interested in gaining more understanding of its clinical applications.

Aparna Baxi Johns Hopkins University
Daniel Biocini Santa Clara Valley Medical Center
Andrew Bryan University of Washington
Adam Burke Imperial College, London
Sean Campbell University of Virginia Health System
Allison Chambliss Johns Hopkins University School of Medicine
Siaw Li Chan University of Chicago
Esther Cynn Columbia University Medical Center
Lucy Evans University of Sheffield
Matthew Feldhammer Emory University
Mahboobe Ghaedi Yale University
Jessica Gifford Calgary Laboratory Services
Nazar Haddad Basrah Medical College
Ronald Henriques University of North Carolina
Ventzislava Hristova Johns Hopkins School of Medicine
Waddah Katrangi Mayo Clinic
Praveen Kumar Beaumont Health System
Zaiping Liu IWK Health Centre, Dalhousie University
Sheng-Ying Lo University of Washington
Mei Lu Biochemical Genetics Laboratory, Icahn School of Medicine at Mount Sinai
Pierre-Luc Mallet University of Sherbrooke
Maximo Marin The University of Chicago Medical Center
Michael Mbughuni Mayo Clinic
Mitchell McGill Washington University School of Medicine
Garrett Mullins University of Virginia
Mahesheema Na Cleveland State University
Belkiz Ongen Acibadem
Jennifer Powers Georgia Institute of Technology
Abraham Qavi Washington University in St. Louis, Barnes-Jewish Hospital
Molly Resnick Connecticut College
Maria Stella Ritorto Memorial Sloan Kettering
Jesse Seegmiller University of Minnesota
Lusia Sepia-Ccovvilley Mayo Clinic
Tujin Shi Pacific Northwest National Laboratory
Brelan Smith University of California, San Diego
Theresa Swift University of Michigan Health System
Awet Teclab Memorial Sloan Kettering Cancer Center
Xander van Wijk University of California, San Francisco
Joseph Wienecke Vanderbilt University School of Medicine
Clayton Wilburn Houston Methodist Hospital
Jane Yang University of California, San Diego
Zahra Yi Dartmouth-Hitchcock Medical Center/ Dartmouth College
Min Yu University of Virginia
Exhibits Summary

The Exhibits officially open at 6:00 PM on Monday with the Opening Reception in the Exhibit Hall in Oasis 1&2. Exhibits will also be open for viewing from 10:30 AM to 7:00 PM on Tuesday and Wednesday.

Below is the Exhibit schedule that also includes events intended to provide focused opportunities for attendees to visit the Exhibits during the Conference.

<table>
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<th>Monday</th>
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<tbody>
<tr>
<td>9:00 am – 4:15 PM</td>
<td>Exhibitor Set-Up (EXHIBITS CLOSED) – Poster Placement for Sunday Presenters Allowed.</td>
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<tr>
<td>6:00 – 8:30 PM</td>
<td>Opening Reception in Exhibit Hall</td>
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<td>Tuesday</td>
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<tr>
<td>10:30 – 11:30 AM</td>
<td>AM Coffee Break in Exhibit Hall</td>
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<tr>
<td>12:30 – 2:00 PM</td>
<td>Lunch provided in the Exhibit Hall.</td>
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<tr>
<td>3:00 – 4:00 PM</td>
<td>Posters in Exhibit Hall</td>
</tr>
<tr>
<td>3:00 – 4:00 PM</td>
<td>PM Coffee Break in Exhibit Hall</td>
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<tr>
<td>5:00 – 7:00 PM</td>
<td>Reception in Exhibit Hall</td>
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<tr>
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<tr>
<td>10:45 – 11:30 AM</td>
<td>AM Coffee Break in Exhibit Hall</td>
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<tr>
<td>12:30 – 2:00 PM</td>
<td>Lunch provided in the Harbor Foyer.</td>
</tr>
<tr>
<td>3:00 – 4:00 PM</td>
<td>Posters in Exhibit Hall</td>
</tr>
<tr>
<td>3:00 – 4:00 PM</td>
<td>PM Coffee Break in Exhibit Hall</td>
</tr>
<tr>
<td>5:00 – 7:00 PM</td>
<td>Reception in Exhibit Hall</td>
</tr>
<tr>
<td>7:00 PM</td>
<td>END OF EXHIBITS</td>
</tr>
<tr>
<td>Midnight</td>
<td>Deadline for removal of Exhibits from Exhibit Hall</td>
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</tbody>
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Exhibitors

**Agilent Technologies** Booth #26-27
Agilent Technologies delivers premiere analytical technologies for clinical research ensuring your success from sample prep to final answer. These include a comprehensive portfolio of innovative automation, chemistries, GC, GC/MS, ICP/MS, LC, and LC/MS solutions which enables the identification and quantification of both endogenous and exogenous substances in complex biological matrices with the utmost accuracy and reliability. Coupled with our dedicated global support network, we will get you to your final answer with minimal ramp-up and maximum productivity.

**ALIFAX** Booth #38
http://www.alifax.com/
ALIFAX was founded in 1988 for the development of innovative solutions in hematology, microbiology, serology and autoimmunity fields becoming rapidly a global important player in the IVD market with 26 active patents, more then 10,000 installed instruments and 1 bln tests sold worldwide. Alifax Eureka LabDivision recently introduced a brand new ready to use CE-IVD line for Liquid Chromatographs, Gas Chromatographs and Mass Spectrometry platforms for Clinical Chemistry, Pharmacology, Occupational/Forensic Toxicology and Endocrinology Therapeutic Drugs Management applications. The mission is to design, produce and support globally the widest kits range fully compatible with the most popular GC/UHPLC/MS/MS manufacturers.

**Apricot Designs** Booth #58
http://www.apricotdesigns.com
Apricot Designs specializes in purpose-built equipment providing innovative, accurate, and precise liquid handling technology that reflects the increasing complexity and requirements of biotech, clinical, and pharmaceutical research. As liquid handling experts and specialists in multi-channel micro-volume pipettors, disposable pipette tips, and high-performance evaporators, we focus on the lab automation needs of researchers, scientists and lab professionals worldwide with equipment designed to make lab work more accurate, more precise, more efficient and thus, more productive.

**Biotage** Booth #59
http://www.biotage.com/
Biotage is a leading provider of sample preparation instrumentation and consumables for a wide range of applications, including pharmaceutical, clinical, forensic, environmental, and agrochemical/food. ISOLUTE® and EVOLUTE® brand solid-phase extraction (SPE) and Supported Liquid Extraction (SLE) products can be run in either a manual or automated environment. The new RapidTrace+ SPE workstation and TurboVap® Solvent evaporators are ideal for increasing throughput and achieving accurate results. Stop by our booth for the latest innovations and applications for Evaporation and Sample preparation.

**Bonna-Agela Technologies** Booth #03
http://www.bonnaagela.com
Bonna-Agela Technologies is a separation technology company that serves chemists and biochemists in the field of drug discovery, food analysis, drug testing, environmental analysis and chemical research. We offer a full line of products designed to meet your separation and purification needs from bulk separation media to chromatography columns and SPE cartridges. Through continuing innovation, Bonna-Agela Technologies Inc. offers customers the best tools and solutions for separation, purification, and analysis of organic and bioorganic compounds. Through our unique nano-surface modification technology, we have developed Venusil HPLC columns and Cleanert solid phase extraction media having incredibly improved surface properties (e.g., less tailing, higher recovery and larger sample capacity).

**Bruker Daltonics** Booth #47
http://www.bruker.com
Bruker Corporation is a leading provider of Chromatography and Mass Spectrometry instruments and solutions for the Analytical Sciences. Our innovative and easy-to-use product families (ESI-QTOF, Ion Trap, FTMS, MALDI-TOF, LC-Triple Quads and GC-Triple Quads) provide the highest performance, ruggedness and value for a wide range of applications in the food, environmental, forensic, industrial, pharmaceutical, and life science research markets
Cambridge Isotope Laboratories Booth #28
http://www.isotope.com
Cambridge Isotope Laboratories, Inc. is the world leader in the manufacture and separation of stable isotopes and isotope-labeled compounds. CIL offers highly pure compounds that are uniformly or selectively enriched in 13C, 15N, D, 18O or 17O. CIL’s labeled reagents are used in proteomics, metabolomics, metabolism, and environmental applications for quantitative mass spectrometry. Our products include MRM PeptiQuant™ assay kits, SILAC protein quantitation kits, media and reagents, 99% enriched amino acids, MouseExpress® Lys 13C6 and 15N mouse feed and tissue, 15N spirulina, intact labeled proteins, growth media for protein expression, cell-free protein synthesis products, environmental contaminants standards for ultratrace analysis, steroids, acylcarnitines, drug metabolites, nucleic acids, lipids and carbohydrates. CIL has GMP capabilities; a majority of substrates can be manufactured to Q7A compliance.

Cayman Chemical Booth #54
http://www.caymanchem.com
Cayman Chemical has over 35 years of experience in producing highly pure analytical standards. Our scientists are experts in the synthesis, purification, and characterization of biochemicals ranging from endogenous metabolites - including complex biolipids, fatty acids, endocannabinoids, and sphingolipids - as well as small drug-like heterocycles. Bulk, custom, labeled standards, and custom mixtures are also available.

Cerilliant Booth #31-32
https://www.cerilliant.com/
Analytical Reference Standards & Certified Spiking Solutions®-Cerilliant offers over 3,000 catalog standards (labeled & unlabeled) including Drugs (pharmaceutical, OTC, & TDM such as hormones, steroids and immunosuppressants), Vitamins, Phytochemicals, Nitroglycerin & by-products, and Environmental Contaminants. Custom services include synthesis, analytical certification, packaging & custom Certified Spiking Solutions®. Cerilliant’s accredited to ISO Guide 34 & ISO/IEC 17025 and certified to ISO 13485 & ISO 9001. Our quality system is compliant to ISO 15194 and incorporates cGMP and GLP. A COA is provided with every product. Call 512-238-9974 or visit www.cerilliant.com.

Chrom Tech Booth #57
http://www.chromtech.com
Distributor of Chromatography consumables, instrumentation and supplies. Featuring: Sample Preparation Products, 96 Well Plates for MS, 96-well Multi-Tier™ Micro Plate System with Glass Inserts, Columns, Instrument consumables and replacement parts, Pumps, Gas Generators. Featured Suppliers include: Agilent Technologies, Thermo Scientific, Sigma Aldrich, Idex (Upchurch and Rheodyne), Parker Balston, Hamilton, Restek.

ChromSystems Booth #01
http://www.chromsystems.com
Chromsystems is a leading global company providing ready-to-use reagent kits and supplies for routine clinical diagnostics by HPLC and LC-MS/MS, the latter representing the gold standard for many parameters. Our product portfolio includes complete kits, quality controls and multilevel calibrators, all ensuring highly accurate as well as a cost-effective analysis in the laboratory. They enable any laboratory to introduce HPLC and LC-MS/MS methods into their diagnostic routine without prior technical expertise. Analyses can be started immediately and sample preparations require the minimum of laboratory time. Our products are comprehensively validated, in particular LC-MS/MS methods with all widely used tandem mass spectrometers. They are CE-IVD compliant, satisfying regulatory requirements for the laboratory. We combine these high quality products with an excellent support programme and service for our customers.

Diagenode Booth #44
https://www.diagenode.com/
Diagenode is a leading global provider of complete solutions for epigenetics research and biological sample preparation. We offer innovative Bioruptor® sonication devices and automation instruments, epigenetics reagent kits, NGS library preparation kits, and high-quality antibodies to streamline DNA methylation, ChIP, and ChIP-seq workflows. The Diagenode’s products simplify the protein research process with a portfolio of unique and robust tools to both isolate and analyze proteins. Our protein research products include the Bioruptor® sonication device, protein extraction beads and kits, unique Western blot ladders that can be directly visualized on film, and highly validated antibodies.
**DPX Labs** Booth #30  
http://www.dpxlabs.com/
At DPX Labs we believe that your sample preparation should be fast and easy. That is why we have incorporated the benefits of solid-phase extraction into a simple to use pipette tip. The patented Dispersive Pipette Extraction (DPX) tip functions by dispersive SPE, requiring only seconds of mixing within the DPX tip to complete the sample preparation process. Now anyone can rapidly extract samples with high recoveries prior to LC/MS analysis. Whether your laboratory uses a single channel pipettor or a fully robotic liquid handler, there is a DPX tip compatible with your analysis method and throughput. Contact DPX Labs so we can help you eliminate matrix interferences and make ion suppression a thing of the past.

**EMD Millipore** Booth #33  
http://www.emdmillipore.com
EMD Millipore provides the innovative solutions you need to advance your research, and more importantly, the support and expertise to utilize them successfully in your lab. You’ll identify more than analytes, target molecules and contaminants. Our full range of water purification products provides accurate lab results, high reliability, low maintenance, predictable and economical running costs and total support. In cellular analysis, protein detection, separation science and membrane filtration, we continue to set the standard for analytical research by providing the highest quality bioanalysis platforms, sample preparation solutions, essential biochemicals, and analytical separation tools.

**GERSTEL** Booth #04  
http://www.gerstelus.com
40+ Years of Chemical Analysis Solutions: GC/MS, LC/MS sample introduction and stand-alone workstations with the most advanced software control available (MAESTRO). MultiPurpose and PrepStation Autosamplers provide maximum versatility and throughput for liquid injection, SPME, Headspace, ALEX, SPE, dpx®, Dynamic HS, ATEX weighing, centrifugation, and SBSE. Twister® performs solventless extraction and ultra-low detection limits. The most versatile Thermal Desorption System available for all sample types. Cooled (PTV) inlet, Olfactory Detection, Multidimensional Heartcutting, Preparative Fraction Collector.

**Golden West Diagnostics** Booth #60  
http://www.goldenwestdiagnostics.com
Golden West Diagnostics, Inc. addresses the need for quality, cost effective biological raw materials for the development of immunoassays and LC-MS applications. GWD provides manufacturers and laboratories with over 80 products including Vitamin D free human serum, serum for ultra-sensitive testing, HSA, HGG, and RGG. Please visit us at www.goldenwestdiagnostics.com.

**Hamilton Robotics** Booth #07  
http://www.hamiltonrobotics.com
Hamilton Robotics is dedicated to the design and manufacture of automated liquid handling workstations. We offer a several types workstations for direct sale and OEM. Key to our products is our air displacement pipetting and monitoring technology as well as the software controlling our systems. We believe every laboratory automation project is unique. Our workstations and software serve as a common high precision and flexible base upon which to provide automated solutions. To this end we employ teams of highly skilled and experienced application and hardware customization specialists around the world to provide our customers with unique solutions to automate their assays successfully and within budget. Please come explore our products and contact us to discuss your automated liquid handling needs further.

**Imtakt USA** Booth #55  
http://www.imtaktusa.com
We are advancing HPLC science by creating unique columns with novel chemistries that provide enhanced selectivity and resolution. We offer a wide range of innovative stationary phases compatible with HPLC, UPLC and LC-MS. Our columns have 25-50% lower pressure and excellent batch-to-batch reproducibility. For more information, please visit our website to view our Product Guide and Application Library.
**Indigo BioAutomation** Booth #50
http://www.indigobio.com/
Indigo BioAutomation has changed how both industry and academic scientists utilize Mass Spectrometers. Its flagship software, ASCENT, is a next generation CDS, that automatically picks and integrates peaks with incomparable accuracy. Indigo BioAutomation is committed to developing computational tools that deliver better science.

**Integrated Micro Chromatography Systems (IMCS)** Booth #29
http://www.imcstips.com
Integrated Micro-Chromatography Systems, LLC (IMCS) is a biotechnology company committed to delivering high impact products to the healthcare industry. At IMCS we believe that personalized medicine is the next frontier in biomedical sciences. IMCS will tackle this frontier by improving existing analytical methods and seeking creative solutions that integrate novel approaches. Product applications that address this need include IMCSzyme®, a purified beta-glucuronidase. Other product applications include IMCStips™. IMCS reverse phase pipette tips are based on a patented SPE technology. The tips contain loosely packed sorbent material inside to combine efficient and rapid extractions. Visit IMCS at booth #29 to learn how to achieve greater recoveries in your hydrolysis, your DNA extraction or your protein purification.

**Ion Bench / MS Noise** Booth #51
http://www.ionbench.com/
IonBench provides furniture for mass spectrometry and HPLC. On display is our IonBench for mass spectrometry, showing industry leading sound suppression, anti-vibration, and space savings advantages of the bench. Custom sizes, features and options make IonBench the first choice for any mass spectrometer installation. IonBench manufactures IonBench LC, elevator benches that enable safer operation and maintenance of stacked HPLC/UPLC systems by electrically raising and lowering the work surface. IonBench LC is transportable, providing versatility, including the ability to connect the HPLC as close to the source as possible. MS Noise manufactures enclosures for vacuum pumps, water chillers, nitrogen generators, and more. Guaranteed sound suppression is 15 dBA, or about 75%. The booth is staffed by FarHawk Marketing Services, distributors for IonBench and MS Noise products in North America.

**IsoSciences** Booth #56
http://isosciences.com/
IsoSciences, LLC is a world leader in the synthesis of stable isotope labeled vitamins, steroids, drug substances, metabolites and other compounds of interest. IsoSciences is ISO9001 certified and has an extensive catalog of stable isotope labeled standards available for immediate delivery both as solids and as CertiMass™ exact concentrations solutions. IsoSciences has added over 200 new products over the past year including an extensive range of 13C3 labeled steroids, Vitamin D metabolites, 13C7-Vitamin B12, 13C6-Vitamin K2 MK4, MK7 and MK9. Contact info@isosciences.com for any internal standard needs you may have!

**ITSP Solutions** Booth #08
http://www.ITSPsolutions.com/
ITSP Solutions, Inc. (Instrument Top Sample Prep) is a completely unique form of Solid Phase Extraction offering precise flow control allowing separations to be performed at their Van Deemter optimum velocity conditions. This yields separation performance that is difficult to achieve with other SPE approaches. ITSP uses the LC/MS/MS autosampler to prepare samples using Solid Phase Extraction and Filtration to reduce labor, increase throughput and enhance the reliability of the analytical instrument. ITSP has methods to test Prescribed and Abused Drugs, Vitamin D, Immunosuppressants, and other compounds. ITSP Solutions’ (booth 8) to discuss how ITSP can benefit your lab.
LGC Standards Booth #24
http://www.lgcstandards.com
LGC Standards (www.lgcstandards.com) provides products and services to improve measurement and quality control within the laboratory, and is part of LGC, whose LGC Science & Technology Division acts as the UK National Measurement Institute for chemical and bioanalytical measurements. LGC Standards supplies over 100,000 products, including reference materials, pharmaceutical impurity reference standards (produced under ISO Guide 34 accreditation), biological standards and reagents, and proficiency testing. LGC Standards is headquartered in Teddington, Middlesex, UK. Its global centre for excellence in proficiency testing is located in Bury (Greater Manchester). LGC Standards has offices in Brazil, France, Germany, Italy, Poland, South Africa, Spain, Sweden, China, Russia, United Arab Emirates, UK and the US, a joint venture presence in India, and representatives in Bulgaria, Czech Republic, Finland, Hungary, Ireland, the Netherlands, Romania and Turkey.

MAC-MOD Analytical Booth #10
http://www.mac-mod.com
MAC-MOD's mission statement is "Smarter Chromatography." But, you may ask, just what does "Smarter Chromatography" mean? It means when we make a recommendation about an HPLC or UHPLC product, it is to partner with you to offer innovative solutions to your complex problems. We use advanced state-of-the-art analytical software to match our product portfolio with your separation needs. We leverage our 30 plus years of technical expertise and manufacturing network to help you solve your toughest application problems. We provide up-to-date and accurate technical catalogs and reports from industry leading separation scientists to keep you informed of new technologies. That is what "Smarter Chromatography" means. Stop by Booth #10 to speak to one of our Chromatography Specialists to discuss our exciting promotions and innovative technologies!

Metabolomic Technologies Booth #16
http://www.metabolomictechnologies.ca/
Metabolomic Technologies Inc. (MTI) is a spin-off company from the University of Alberta in Edmonton, Alberta, Canada. Established in 2010, MTI is a privately owned company and sole owner and proprietor of PolypDx™. Formed from a research program facilitated by Drs. Haili Wang and Richard Fedorak, who were interested in using metabolomics to explore how colorectal cancer, a leading cause of cancer deaths in North America but curable if identified early, affected cellular metabolism. PolypDx™ is a spot urine diagnostic test to detect adenomatous (precancerous) polyps, and advances the prevention of CRC. Focused on driving novel research findings to commercial products, MTI specializes in metabolomic-based diagnostics for the healthcare market. MTI received the 2014 North American Frost & Sullivan Award for Technology Innovation Leadership.

mSPEC Group Booth #49
http://www.mspecgroup.com
We believe that products and relationships should be built to last, that knowledge should be shared and innovation should benefit everyone. Under the umbrella of mSPEC group of companies we have been supporting the mass spectrometry industry since 1996, offering a wide range of ISO certified comprehensive maintenance, application and production support programs designed to meet your needs, however unique they may be. Specialized in: - Method development, validation & application support -Full service coverage, preventative maintenance & repairs -Staff proficiency training and production support -Turn-key LCMS laboratory instruments, accessories and consumables mspecgroup.com msparts.com

Neoteryx Booth #17
http://www.neoteryx.com
Neoteryx delivers automatable and quantitative microsampling solutions comprising of technologies for minimally invasive, economical specimen collection and transportation, facilities for designing/manufacturing custom remote sampling kits, and services that include extraction method optimization, analytical method development, and turnkey workflow installations.
New England Peptide Booth #43
http://www.newenglandpeptide.com/
New England Peptide (NEP, Gardner, Massachusetts) has designed and produced high quality custom peptides, polyclonal and monoclonal antibodies for research organizations worldwide since 1998. Our chemists and immunological experts have over 100 years of experience and deliver a full range of peptide and antibody services for biotech and pharmaceutical applications. These include custom peptide synthesis, custom peptide arrays, polyclonal antibodies, quantitative proteomics via our NEPTune™ platform, and analytical services such as mass spec and AAA. Learn more at www.newenglandpeptide.com.

Obotics Booth #18
http://www.obotics.net
Obotics is changing the way you interact with lab automation. For pre-chromatographic/MS analysis, we believe there's nothing more comprehensive and well-suited for your automated sample prep then OB-1 from Obotics. OB-1 automates literally every type of sample prep utilized for Mass Spec analysis. Beyond that, what users really love is that there is NO PROGRAMMING REQUIRED to have OB-1 go to work for you. With an intuitive user interface, requiring only the most basic information like how many samples, volumes of reagents required, length of time for positive pressure to process SPE plates and cartridges...OB-1 will change the way you think about lab automation. We are excited to visit with you and learn about your applications where you want to improve both workflow efficiency as well as precision and accuracy.

Optimize Technologies Booth #22
http://www.optimizetech.com
Optimize Technologies offers a complete line of innovative components and replacement parts for UHPLC, HPLC and LC/MS systems. Products include EXP® Fittings, Filters, Traps and Guards, OPTI-MAX® Check Valves, OPTI-SEAL® Seals, Replacement Pistons, OPTI-GUARD® Guard Columns, OPTI-PAK® Traps, OPTI-SOLV® Filters and OPTI-LYNX™ Quick-Connect packed beds. New products include EXP® hand-tight fittings, UHPLC/MS traps, UHPLC filtration, guard solutions rated to 20,000+ psi and OPTI-TRAPS™ for large molecules, peptides, online desalting and detergent removal. All Optimize EXP® products feature hand-tight holders and EXP® Titanium Hybrid reusable ferrules.

OraSure Technologies Booth #13
http://www.orasure.com
OraSure Technologies manufactures oral fluid devices and other technologies designed to detect or diagnose critical medical conditions. Its innovative products include rapid tests for HIV and HCV antibodies, influenza antigens, testing solutions for detecting drugs of abuse, and oral fluid sample collection, stabilization and preparation products for molecular diagnostic applications.

Orochem Technologies Booth #48
http://www.orochem.com/
Established in 1996, Orochem Technologies Inc. manufactures unique Sample Prep and Chromatography Products for the Bioanalysis, Drug Discovery, and the Genomics and Proteomics markets. Backed with unique expertise in high throughput formats, membranes and surface chemistries, Orochem was one of the first companies to translate the concept of pre-filters from single to high throughput formats, a concept now widely implemented for sample prep plates in the biotech and analytical markets. In the year 2001 Orochem manufactured the first commercially available Protein Crash and Precipitation 96-well plate for Bioanalytical processes. Orochem Technologies serves the clinical diagnostic labs in the areas of drugs of abuse, steroids, vitamin D and metabolites, and proteomics. At this MSACL, we will present our new vitamin D Metabolite Extraction Kit, and new HPLC columns for steroid isomer separation.

Parker Hannifin Booth #09
http://www.parker.com/fns/balstonlabgasgenerators
Our company manufactures high efficiency gas generators to eliminate high pressure cylinders from the laboratory. Gas generators provide increased safety, free up laboratory space, save money and produce ultra high purity gasses for your laboratory instruments. With a gas generator you are in control. These state-of-the-art gas generators continuously produce ultra-high purity gases for LC/MS, GC, FT-IR, TOC, ICP, AA and other instrumentation. All products are backed by fully staffed field sales and service organizations and one-year warranty. Preventative maintenance programs and extended warranties are available for all Parker Balston products.
Phenomenex Booth #46
http://www.phenomenex.com
Phenomenex is a global technology leader committed to developing novel analytical chemistry solutions that solve the separation and purification challenges of researchers in industrial, government and academic laboratories. Phenomenex’s core technologies include products for liquid chromatography, gas chromatography, sample preparation, bulk purification chromatographic media, and chromatography accessories and equipment. For more information, visit www.phenomenex.com.

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Phytronix Technologies Booth #45
http://www.phytronix.com/
The leader in quantitative ultra-fast high-throughput analysis for mass spectrometry presents the LDTD-96 and LDTD-384 ion sources. These platforms represent a unique shotgun approach that introduces the sample into the mass spectrometer using an ultra-fast Laser Diode Thermal Desorption (LDTD®) process. The LDTD Ion Source technology is a unique solution to increase sample analysis throughput for your application needs.

Promega Booth #37
http://www.promega.com
Contributing to Science, Discovery and More. Founded in 1978, what started as the production of enzymes for researchers has evolved to offering over 3,000 products for a broad array of applications including basic research, drug discovery, forensics and paternity testing, and molecular diagnostics. Quality Mass Spec Grade reagents like Trypsin Gold and Trypsin/Lys-C Mix assure consistent, reliable results in mass spec applications.

Prosolia Booth #23
http://www.prosolia.com
Prosolia’s DESI, Flowprobe and Velox 360 products empower scientists in the pursuit of obtaining better chemical data for better decisions in science and medicine. Our portfolio of scientific analytical tools includes innovative sample introduction systems and intuitive software - all of which are part of workflows that reduce complexity and accelerate results.

RECIPE Chemicals & Instruments Booth #25
RECIPE was founded in Munich, Germany, in 1982 and is one of the leading companies in HPLC and LC-MS/MS diagnostics today. For mass spectrometry, RECIPE offers CE/IVD labelled ClinMass® LC-MS/MS Complete Kits. Furthermore, several reagents such as ClinMass® Optimisation Mixes and Internal Standards, ClinCal® Calibrators and ClinChek® Controls are available for a reliable and standardised LC-MS/MS analysis. All products are developed and produced in our state-of-the-art production plant in Munich. RECIPE is recognised worldwide as a reliable partner for clinical laboratories and is certified by the quality management standards ISO 9001 and 13485.

Restek Booth #19
http://www.restek.com
A leading innovator of chromatography solutions for both LC and GC, Restek has been developing and manufacturing columns, reference standards, sample preparation materials, accessories, and more since 1985. We provide analysts around the world with products and services to monitor the quality of air, water, soil, food, pharmaceuticals, chemicals, and petroleum products. Our experts have diverse areas of specialization in chemistry, chromatography, engineering, and related fields as well as close relationships with government agencies, international regulators, academia, and instrument manufacturers. www.restek.com
SCIEX Booth #05  
http://sciex.com/applications/clinical-research

SCIEX helps to improve the world we live in. SCIEX LC-MS/MS solutions enable clinical researchers to push the limits of analysis across a wide variety of applications, including quantitation of steroids, vitamin D, immunosuppressants or drugs of abuse, by harnessing the power of mass spectrometry through exceptionally simple-to-use tools. SCIEX offers the most comprehensive portfolio of pre-configured LC-MS/MS methods and software for clinical research and toxicology. All based on the proven reliability of SCIEX systems, including the SCIEX QTRAP® 5500 system, the most sensitive LC-MS/MS system for trace level analysis -- all backed by the most comprehensive service and support organization in the industry. For more information, go to www.sciex.com/clinicalresearch

SECTRA Booth #52  
http://www.sectra.com

Over the last ten years, new technology has enabled pathology departments to begin digitizing their work. Based on this trend, Sectra has developed Digital Pathology Solutions for the next generation consisting of a high-end diagnostic viewer, unified integrations, and proven archiving and image handling protocols. With full focus on end-user experience and workflow efficiency, pathologists are able to make their diagnoses and reporting faster and easier through efficient image interaction, access to full case overview any time, from anywhere, as well as easy image sharing for external review and a balanced workload.

Scientific Systems Booth #53  
http://www.ssihplc.com

Scientific Systems, Inc. (SSI) designs and manufactures a full line of high performance piston pumps and fluid path components for HPLC, Precision Metering and Process applications. Flow rates range from 1 micro-liter to 300 ml/min, with pressures up to 25,000 psi. Fluid paths are offered in PEEK, Stainless Steel and Titanium, in a wide variety of single piston and dual piston platforms. All SSI pump products are available as stand-alone units or as customized kits for OEM instruments. Since 1967, SSI has provided innovative products to the laboratory and industrial markets, with the highest level of Quality and Customer Service.

Shimadzu Booth #39-40  
http://www.shimadzu.com/

Founded in 1875, Shimadzu is a multinational corporation with three major divisions: Medical Diagnostics, Aerospace/Industrial, and Analytical Instruments. The Analytical Division is one of the world’s largest manufacturers of analytical instrumentation, supporting a broad range of applications including life sciences, pharmaceuticals, food safety, environmental, chemicals, and forensics. Shimadzu expanded the scope of its ISO-13485 certification, which covered blood coagulation and automatic clinical chemistry analyzers, to include LCMS and LC instruments. Shimadzu will continue to register medical devices with the FDA, and support the growing demand for LC and LCMS in clinical testing markets. Visit our booth to learn more about new Shimadzu platforms, including our ultra-fast LCMS-8050 triple quadrupole, automated protein digestion workstations and a “lab-on-a-card” technology that generates volumetric plasma from an unmeasured drop of whole blood in minutes.

Sigma-Aldrich Booth #15  
http://www.sigmaaldrich.com/united-states.html

Sigma-Aldrich, a leading Life Science and High Technology company, offers a variety of solutions designed to meet the needs of clinical and forensic scientists. The combined expertise from Sigma-Aldrich, Supelco and Cerilliant create a complete solution for the mass spectrometry-based toxicology workflow. This portfolio of tools includes high quality reagents, analytical products and certified reference materials. Our commitment to high quality and reliable delivery is always focused on accelerating our customers’ success by ensuring that our products do not interfere with results and keep the laboratory running smoothly.

SimulTOF Booth #20  
http://simultof.com/

We are introducing our new SimulTOF ONE MALDI-TOF at MSACL 2016. This is a true desktop instrument with patented technology that provides higher sensitivity and resolving power than even much larger, more expensive instruments. A high resolution video camera reads bar codes on the sample plates and provides real-time images for controlling automated acquisition and processing of data. Operation at 1 kHz is standard and 5 kHz and 20 kHz operations are optional. Other options include bipolar operation and a simple, very fast autoloader that transfers sample plates from atmosphere to the ion source in less than 20 seconds.
**SPEware** Booth #06  
http://www.speware.com  
SPEware Corporation brings advanced separation efficiency to the extraction laboratory using micro-particulate Solid Phase Extraction (SPE) paired with Positive Pressure Manifolds. We have 20 years of experience designing, manufacturing and providing Positive Pressure Processors directly to our customer and to resellers. As the original equipment manufacturer, we have perfected the technology of positive pressure for use with our micro-particulate products as well as developed fully automated extraction procedures. SPEware specializes in customized solutions ranging from traditional extraction problems to unique issues that require a high degree of purification and efficient processing. We strive to provide superior customer service and quick turnaround times. We offer a team of experts that includes our scientific advisory board, analytical chemists, and field application scientists in order to deliver innovative solutions to your SPE needs.

**Tecan** Booth #36  
http://www.tecan.com  
Tecan is a leading global provider of laboratory instruments and solutions in biopharmaceuticals, forensics, and clinical diagnostics. Had enough of tedious mass spectrometry sample preparation? Tecan offers Freedom EVO®-based end-to-end process automation for even the most challenging protocols, liberating you from the bottleneck of manual sample preparation. Keep up with ever-increasing demands with Tecan Freedom EVO • Solid phase extraction • Liquid liquid extraction • Protein purification AC Extraction Plate™ The Tecan AC Extraction Plate with TICE™ (Tecan Immobilized Coating Extraction) technology revolutionizes your sample preparation routine. A simple pipette and shake sequence, with no filtration, centrifugation or solvent evaporation, is all that is required. The AC Extraction Plate is easily integrated into automated processes, making it a perfect match with Tecan’s Freedom EVO® liquid handling platform.

**Teledyne CETAC Technologies** Booth #41  
http://www.cetac.com  
A worldwide leader in sample introduction and sample handling equipment for elemental analysis. Teledyne CETAC Technologies provides a comprehensive range of product based solutions for the analysis of elements in samples ranging from drinking water and high purity acids to radioactive waste. Our spectroscopy and automation groups develop, manufacture and market a family of products and services for customers around the world, for use in every industry where rapid and accurate determination of trace element concentrations is required.

**Thermo Scientific** Booth #34-35  
http://www.thermoscientific.com  
Innovation applied to clinical research and forensic toxicology. Look to Thermo Scientific for continuous innovation in clinical research solutions, including mass spectrometry, chromatography, automated online sample preparation, multiplexing, software and consumables. Whether your lab is large or small. Whether your need is to analyze small molecules or proteins. We have the expertise, products and flexibility to supply the right answer.

**Thomson Instrument Co.** Booth #02  
http://htslabs.com/  
Thomson Instrument Company is a leading-edge manufacturer and supplier of consumable products for the Chemistry and Biological fields. Our SINGLE Step Filter Vials (450uL capacity), Nano Filter Vials (10uL minimum sample volume), and eXtreme Filter Vials (>30% particulates) are used in many labs for all your sample preparation needs and are compatible with most standard autosamplers for HPLC, GC, LC/MS. We provide a number of simple standard and custom products to meet our customer's needs. Please look at our website at www.htslabs.com. We are committed to competitive pricing and quality customer service. Ph: 800-541-4792 or 760-757-8080 Fax: 760-757-9367 E-Mail: folks@htslabs.com

**UTAK Laboratories** Booth #14  
http://www.utak.com  
Since 1973, UTAK Laboratories, Inc., has been connecting Research and Commercial Laboratories with the most comprehensive menu of Stock and Custom manufactured Quality Controls available. Our Products offer complete commutability with many methods of evaluation including: Immunoassay, ELISA, HPLC, UHPLC, ICPMS, GC/MS, and LC/MS, TOF, etc. Our entire line of 100% REAL Human Matrix products along with our Specialty Matrix (SMx™) products come together to offer Laboratorians a true 3rd party Quality Control, especially for Laboratory Developed Tests or LDT’s. Ask us about QC for your LDT. UTAK, createCONTROL
At Waters Corporation, we understand the factors necessary to succeed at each stage of the health sciences continuum, from the challenges of biomarker discovery and translation to validation and commercialization of innovative clinical diagnostics. We draw on first class scientific expertise to bridge the translation gap and help further the understanding and management of disease. Driven by purposeful innovation, we have created a comprehensive line of scientific products and services designed to support the entire continuum of biomedical research. These include state of the art analytical tools such as chromatography and mass spectrometry, associated informatics, and supportive sample preparation and diverse column chemistries. www.waters.com/msacl

Zef Scientific Booth #42  
http://www.zefsci.com  
• Is your Mass Spectrometer showing the uptime that you expect? • Do the different vendors tend to blame each other—or your method—for an issue? • Are you looking for a more harmonized and seamless experience in maintaining your LC-MS/MS? ZefSci is the country’s premier independent LC-MS/MS engineering firm. A network of experienced field service and qualification engineers are strategically positioned nationwide supplying our customers with the highest level of services on AB/Sciex, Thermo, Waters, Agilent, and Shimadzu. 1- Service Contracts 2- Preventative Maintenance 3- Repair 4- GxP Compliance IQ/OQ/PQ
Discussion Groups : Tuesday 7:00 – 8:00 PM

Discussion Groups are non-commercial gatherings that are intended to provide an opportunity for like-minded individuals to get together to share their ideas, create common networks of interest or just have a good time while learning a little bit more about clinical mass spectrometry.

**CDC Standardization Programs Forum**
@ Chino
Lead(s): Hubert Vesper & Julianne Botelho
In memory of Dr. Dr. Karl Siegfried Boos. The discussion group will feature a short “Life in Review” of Professor Karl Siefried Boos's contributions to clinical diagnosis. This will be followed with a "Critical Method Review" competition – specifically highlighting sample preparation, a subject near and dear to Professor Boos.

**Convincing Administrators (and the Public) of the Benefits of MS in the Clinic**
@ Pueblo
Lead(s): Soumen Manna
Assemble highlights for the purpose of creating compelling powerpoint for those new to the field (i.e. clinical lab directors, managers, public). Discuss MS-based methods with respect to their technical and economic superiority/inferiority to the existing/emerging alternatives. Identify examples (if any) existing or emerging diagnostic/prognostic tests where MS is the only viable option. Highlight green aspects comparing environmental footprints (energy, toxic waste, chemical and bio-hazards) vis-a-vis existing techniques. Review evolution and adoption of Clinical MS, explore challenges, ethics, mistakes.

**MSACL Fundamentals Track - What’s Next?**
@ Mojave Learning Center
Lead(s): Robert Fitzgerald & Judy Stone
Feedback on the Fundamentals / Newbies track. How is it going? What can be improved?

**Understanding Patents in Mass Spectrometry**
@ Catalina
Lead(s): Ben Borson
This discussion group will review real world patent claims in the field of metabolite analysis using mass spectrometry and some simpler ‘made-up’ claims to help scientists understand what activities would fall under the experimental use doctrine, direct infringement, indirect infringement, contributory infringement, infringement under the doctrine of equivalents and how to design around infringement of a method or a device claim.

**CSI - MSACL**
@ Madera
Lead(s): Robert Kobelski & Jack Henion
A fun-filled opportunity to apply mass spectrometry tools and talents to solve a case of mysterious exposure to chemicals of medical significance. Crime scene data can include GC-MS results and olfactory clues. Clinical analysis results can include; clinical presentation, symptoms, GC-MS, ICP-MS and/or LC-MS data. This is an opportunity to flaunt your MS interpretation skills in front of your peers.

**Eating A Whale, One Bite At A Time**
@ Pasadena
Lead(s): Russell Grant & Brian Rappold
Yo ho ho mateys’ - it’s time to charge the guns and hoist the mainsail. The evenings' entertainment will focus on bottom up protein assays through finding the flaws in proposed methods. Let the grog flow and battle(ships) commence as we learn how to eat a whale of a "clinical protein" assay.

**Early Career Development Council**
@ Sierra
Lead(s): Jane Yang
To create the opportunity for clinical mass spectrometrists, early in their careers, to assemble with the intent of creating and maintaining an interest group with a discernible voice that will communicate directly and effectively with MSACL, MSACL vendors and the clinical mass spectrometry community at large.
Corporate Workshops: Tuesday 8:00 – 9:00 AM

**Bruker - Chino**

*(1) Advances in MALDI Imaging of Clinical Samples, (2) The Chemistry of the Human Lung Associated with Cystic Fibrosis*

*(1) Jeffrey Spraggins, PhD, Vanderbilt, (2) Pieter Dorrestein, PhD, University of California, San Diego*

‣ (1) In recent years, instrumentation for imaging mass spectrometry has reached unprecedented speed and sensitivity. Bruker’s rapifleX MALDI Tissuetyper, a next-generation MALDI TOF mass spectrometer was designed for imaging on clinical timescales. This presentation will review some significant advances and demonstrate applications for the imaging of clinically important tissue specimens.

(2) The microbiome is critical to human health yet we know little about the chemical environment that our microbes live in. In this presentation we will explore untargeted metabolomics strategies to reveal the chemical environment of the microbiome. In this presentation we will highlight the metabolome of a human lung associated with Cystic Fibrosis in 3D and its relationship to medicines, metabolism of medicines and microbes.

**Restek - Pueblo**

**Selectivity Accelerated: Utilizing Raptor™ LC Columns for Clinical Solutions**

*Frances Carroll, Shun-Hsin Liang, Sharon Lupo*

‣ Superficially porous particles (SPP) have been proven to provide fast separations without the need for expensive instrumentation, thereby increasing sample throughput without capital investment. Although column efficiency considerably accelerates analysis time, it has little effect on resolution. Conversely, selectivity has a substantial impact on resolution, but shows minimal improvement in analysis times. By being the first to combine the speed of SPP with the resolution of Restek’s unique Ultra Selective Liquid Chromatography technology, Raptor™ LC columns provide the practicing analyst with the most powerful tools available for fast and efficient method development. This workshop will discuss how to capitalize on the selectivity of Raptor™ LC columns in challenging clinical analyses by providing application examples.

**Waters - Mojave Learning Center**

**Towards Standardization in Protein Quantification Workflows**

*Paula M. Ladwig, MS, MT(ASCP); Development Technologist Coordinator with Department of Laboratory Medicine & Pathology at Mayo Clinic in Rochester MN, Mary Lame, Senior Applications Scientist, Waters Corporation*

‣ This workshop highlights the implementation and benefits of generic, kitted methods used to simplify, streamline, and standardize common protein quantification workflows, while reducing variability and delivering accurate and precise results. Data for infliximab, adalimumab, trastuzumab, bevacizumab, and the antibody drug conjugate T-DM1 will be shown as working examples. For full abstract go to: www.waters.com/msacl
Corporate Workshops: Tuesday 2:00 - 3:00 PM

Thermo Scientific - Mojave Learning Center

Alternate Sample Preparation Approaches for Your Mass Spectrometry Clinical Research Assays
William Clarke, PhD, The Johns Hopkins University School of Medicine

- The first part of this session will focus on the research of cell disintegrated blood (CDB) as a matrix for the analysis of immunosuppressant drugs. Opportunities, challenges, and limitations of CDB will be explored. The second part of this session will focus on alternate sample preparation approaches for the analysis of dried urine spots. Research analysis of field samples from HIV prevention trials compared to research analysis of liquid urine will be discussed, as well as other potential opportunities and limitations of the methodology.

SCIEX - Catalina

Development of High Sensitivity MicroLC-MS/MS Method for Estradiol Research in Human Serum Without Derivatization
Jerry Yeo, PhD, Xin Yi, PhD

- During this presentation, we will discuss the technical challenges of developing high sensitivity LC-MS/MS methods for estradiol in blood, how to improve sensitivity and reduce ion suppression for estradiol on MicroLC-MS/MS system, and discuss the advantages and disadvantages of using microLC system versus normal flow LC system.

Neoteryx - Madera

3 Unique Talks Regarding the Application and Benefits of Integrating Volumetric Absorptive Microsampling (VAMS) into the Clinical Lab – 1) Automated, Bottom-up Proteomics Workflow; 2) LC-MS/MS Assay for Immunosuppressant Monitoring; 3) Monitoring of Therapeutic Drug by LC-MS/MS and Diagnostic Biomarkers by ELISA
1) Irene van den Broek, Ph.D., Research Scientist for Advanced Clinical Biosystems Research Institute at Cedars-Sinai Medical Center; 2) Paul J. Jannetto, Ph.D., Director of Toxicology and Drug Monitoring Laboratory at Mayo Clinic; 3) Ying Qu, Ph.D., Senior Scientist at Exagen Diagnostics

- Talk 1) discusses application of VAMS for protein biomarkers, focusing on the optimization of protein extraction from 10µL of blood & integration into a bottom-up proteomics workflow on an automated liquid handler. Talk 2) will look at feasibility of measuring Tacrolimus and Cyclosporin A with a HPLC-MS/MS assay using dried blood from a VAMS device (20µL) compared to a validated method using 200µL venous collected EDTA whole blood. Talk 3) will review a DBS comparative study (whole blood & red blood cell results) where VAMS (10µL) was applied in monitoring methotrexate polyglutamates (MTXPG1-5) in methotrexate (MTX) treated patients by a LC-MS/MS method as well as discuss how VAMS was used in ELISA based biomarker monitoring of rheumatoid factors (e.g. anti-IgM RF, anti-CCP) used as diagnostic biomarkers for autoimmunological disease.

Thomson Instrument Co - Pasadena

Streamlined Sample Preparation of Biological Samples Using the Thomson Filter Vials & Analysis by LC-MS/MS
Lisa Wanders

- Sample preparation continues to be a critical factor in the quantitative measurement of biological samples. The goal of this seminar is to discuss how to streamline the sample preparation process of oral fluids, urine and blood utilizing the Thomson eXtreme, nano and the eXtractor3D Filter Vials. Reducing interferences from sample matrices and increasing analyte recovery are key requirements for preparing biological samples. Thomson Filter Vials save time, reduce solvent usage, alleviate the need for expensive consumables and lab equipment. Sample preparation for matrices such as urine, blood and oral fluids will be discussed.

SimulTOF - Sierra

New technology for imaging of biological tissues by MALDI-TOF
Stephen Hattan

- This novel approach improves sensitivity, image resolution, data quality, consistency, reproducibility, flexibility, protocol simplicity and cost of analysis for MALDI-IMS. It uses chemically modified µ-channel plates to act as substrates, and simplifies experimental protocol by removing restrictions for cryogenically sliced tissue specimens.
SimulTOF - Chino
Quantitative MALDI-TOF mass spectrometry for clinical applications
Marvin L. Vestal PhD

MALDI-TOF MS is used for analyzing a variety of nonvolatile molecules, but acceptance has been limited by the belief that MALDI-TOF is not quantitative. Results are presented on new MALDI-TOF mass spectrometers that generate reproducible spectra on complex samples. High sensitivity and accurate masses are achieved by operating at laser rates up to 5 kHz and summing up to 500,000 shots/sample. Recent and potential clinical applications are reviewed.

SCIEX - Pueblo
The Lipidyzer: The Convergence of Differential Ion Mobility and Mass Spectrometry to the Next Generation Lipidomics Analysis Platform
Paul Baker, PhD

There is growing interest in characterizing lipid molecular species as clinical biomarkers of human disease. MS-based lipidomics data arrays are processed by lipid ID software followed by PCA to generate candidate lipid biomarkers. This process is challenging due to the numerous lipid isobars that interfere with quantitation. Differential Mobility Spectrometry (SelexION® Technology) coupled to MS analysis is effective at resolving complex lipid mixtures. This technology has been applied to quantitative lipidomics using the LipidyzerTM, which detects and measures over 1200 lipids with absolute quantitation. In this presentation, the application of SelexION® Technology to global and targeted lipidomics will be discussed, and data will be shown demonstrating how it has fundamentally changed the future of lipid analysis.

Thermo Scientific - Mojave Learning Center
Which Chromatography and Mass Analyzer is Right for Your Clinical Research Application?
Lewis Couchman, Kings College Hospital

Mass spectrometry has wide applicability in clinical research, especially when combined with modern chromatography and sample preparation. However, clinical research method development should remain application-centered, and ideally use a range of approaches to design a ‘fit-for-purpose’ methodology. We will describe the applicability of turbulent flow chromatography, high-resolution, accurate mass (HRAM) LC-MS, and rapid quantitative analysis using triple quad mass analyzers. The merits of each will be discussed using examples from clinical research methods.
**Corporate Workshops : Wednesday 2:00 – 3:00 PM**

**Waters - Mojave Learning Center**

**The Impact of Evolving LC-MS/MS Technologies upon Clinical Research Methods**

*Tim Wood, Biochemical Genetics Laboratory, Sarah Young, Duke Hospital Biochemical Genetics Lab*

- As the performance of all aspects of LC-MS/MS technology has progressed over the years, clinical research methods have benefited from increasing analytical sensitivity, specificity and throughput. In turn, this has lead to the sharpening of approaches for the detection of disease-specific biomarkers, and ultimately a better understanding of the underlying biochemistry for a number of metabolic disorders. In this workshop, you will hear experiences from two prominent experts in the biochemical genetics community who will describe the effects of evolving LC-MS/MS technology upon their research. For full abstract go to: www.waters.com/msacl

**Phenomenex - Catalina**

1. **Spitting in the Face of your MS, and Why That is a Bad Idea. 2. Automation in the LCMS Laboratory**

*1. Sean Orlowicz, Seyed Sadjadi - Phenomenex 2. Rohit Shroff - Tecan*

- 1. Oral Fluids provide many advantages over more invasive sample collection options, however their LCMS analysis can come with litany of new challenges. In this talk, we focus on overcoming some of these challenges including: sensitivity, matrix effects and the recovery of multiple drug classes, through the use of sample preparation and HPLC techniques. 2. Increasing test volumes of mass spectrometry assays in the clinical laboratories are challenging many to revisit the major bottleneck in their workflows – manual sample preparation. Tecan has developed tailored workflow automation solutions for a variety of clinically important analytes and extraction methodologies to alleviate this bottleneck. In this talk, we will investigate some of the tools available to improve your workflow.

**Biotage - Madera**

**Small Sample Volumes Are Small Problems**

*Kris Franklin, Lite Consulting*

- With advances in LC-MS/MS technology and automated sample preparation, the need for large sample volumes are no longer a requirement for many assays. The sensitivity and specificity of modern LC-MS/MS allows for multi-analyte panels to be targeted, which has the potential to reduce cost for clinical lab operation. The challenge of multiplexing targets into a single LC-MS/MS run is the development of a robust sample prep that sufficiently removes sample matrix and interfering substances or buffers that may harm or reduce sensitivity of the instrument, while maintaining adequate recovery of the targets. Recent developments in our lab have allowed for reduced sample volumes while producing clinically relevant values for both toxicology and endocrinology. This seminar will include several application examples including oral fluids, urine and hormone quantification in whole blood.

**Agilent Technologies - Pasadena**

No summary as of press time.

**Sigma-Aldrich - Sierra**

**Managing Matrix Impact: High -throughput 25-hydroxy Vitamin D Testing with LC-MS/MS with Phospholipid Depletion**

*Judy Stone and Craig Aurand*

- Craig Aurand will cover the impact of phospholipid matrix interference and describe techniques to minimize the impact on LC/MS assays. Judy Stone will describe the development of a high-throughput 25-hydroxy Vitamin D (VITD) clinical assay at the Northern California Kaiser Regional Laboratories. In 2010 their test volume for serum increased 30-40% per year, and by 2011, the lab anticipated receiving 1200-1500 samples a day for this test. Stone will describe the rationale and methodology for use of Hybrid-SPE plates for VITD sample prep to add the analytical and process robustness that was considered critical for such an ambitious change in workflow to succeed. By 2015 the lab was testing for VITD at the max LC-MSMS throughput of 2200 samples a day with this protocol, maintaining excellent performance metrics for accuracy and precision.
Preparing for a full method validation can be a daunting task. Join us to see how the tools & techniques of Project Management can make the process more predictable, more efficient, and more flexible. Example forms will be provided.
EMD Millipore - Chino

#1 - Preparing Clinical Samples for Meaningful Mass Spectrometry (MS) Up to 75% of the work and expenditure of an analytical lab is spent on sample preparation.

Ivona Strug

- Choosing the right sample prep methods tools can improve the MS workflow and save time. Attend our popular workshop on contaminants and matrix components that potentially interfere with MS analysis, and how you can minimize interference with proper sample preparation. Some of the most expensive errors in MS analyses are caused by sample particulates. Particulates are usually removed by filtration, which could introduce further contamination if incompatible or low-quality filter devices are used. Our presentation will focus on practical solutions for sample and solvent filtration--how to choose the right filter and avoid leached contaminants. You will learn tips for simple, fast sample preparation using centrifugal devices (FASP, or filter-aided sample prep). We will also show how to make your processed samples more LC-MS-ready by applying ZipTip® devices.

Hamilton - Mojave Learning Center

: Hamilton Robotics: Innovative High-throughput Sample Preparation Modules for Bioanalytical Analysis

Michael Mouradian, Ph.D. Scientific Leader, Drug Discovery, Hamilton Robotics

- This workshop will discuss Hamilton's automation tools for bioanalytical workflows focusing on clinical laboratories. Workshop highlights will include, new modules for automated mass spectrometry sample preparation and robust sample preparation methods for reliable, high-throughput analysis.

Shimadzu - SmokeTree

Pharmacogenomics- and Therapeutic Drug Monitoring- Guided Treatment for Precision Patient Care.

Kevin Rosenblatt, MD, PhD, CMO, CSO & Lab Director, CompanionDx Labs

- This interactive workshop will take a closer look at the use of genetics, metabolomics and proteomics measurements to suggest more effective patient therapies. Successful integration and reporting of pharmacogenomics and metabolite/’omics data, as well as the development of new MS-based technologies that enable these measurements, will be presented. Advances in ultra-fast single reaction monitoring/multiple reaction monitoring (SRM/MRM), plasma separation cards (noviplex cards, Novilytic Labs) and fully-automated clinical lab automation module (CLAM-2000) technology will be discussed. "Kick Some Mass" t-shirts will be given to the first 70 attendees!
Tuesday @ 11:30 AM in Mojave Learning Center

**Overview of MS Instrumentation**

*Breland Smith* - *University of California, San Diego* (bes003@ucsd.edu)

- Mass spectrometry is a highly sensitive analytical technique with growing importance in the clinical lab. This session will cover the basic principle of mass spectrometry describing the three main components of a mass spectrometer, with a focus on tandem mass spectrometry (MS-MS) and its use in clinical chemistry.

Tuesday @ 11:50 AM in Mojave Learning Center

**Basics: Tuning Your Mass Spectrometer**

*Jane Yang* - *UCSD* (jyy008@ucsd.edu)

- Tuning, which involves mass calibration and mass resolution, is fundamental to operating a mass spectrometer. This overview will introduce basic concepts to empower novice users understand what happens when the mass spectrometer is tuned.

Tuesday @ 12:10 PM in Mojave Learning Center

**Compound Specific Tuning**

*Imir Metushi* - *UC San Diego Health* (imetushi@ucsd.edu) -- *Young Investigator Grantee*

- Compound specific tuning is essential in order to develop a quantitative LC-MS/MS based multiple reaction monitoring assay. This overview will focus on compound specific tuning and introduces basic concepts to help novice users understand what it means when your instrument representative says “We need to tune the mass spectrometer for your compound”.

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Tuesday @ 11:30 AM in Catalina

**Investigating Serum Metabolites as Circulating Biomarkers of Occupational Exposure to the Artificial Butter Flavoring Compound 2,3-butanedione**

*J. Will Thompson - Duke University* (will.thompson@duke.edu)

- Occupational exposure to diacetyl (butanediol) vapor, utilized as artificial butter flavoring, has been shown to induce fibrotic lung disease called bronchiolitis obliterans (BO), yet there are no methods to monitor chronic occupational exposure. In an effort to develop a group of circulating biomarker of occupational exposure, two separate quantitative metabolite methods were utilized to profile plasma from rats exposed to 125 mg/kg diacetyl or sterile H2O as a control via intratracheal instillation. A number of putative biomarkers of DA exposure were apparent in the plasma, including increases in long chain acylcarnitines, differentiation in a marker of oxidative stress (Met:Met-SO ratio), and decrease in proline:lysine ratio.

Tuesday @ 11:50 AM in Catalina

**Abiraterone Metabolism in Castration Resistant Prostate Cancer**

*Mohammad Alyamani - Cleveland State University* (m.alyamani@vikes.csuohio.edu) -- *Young Investigator Grantee*

- Advanced prostate cancer is the second leading cause of cancer-related deaths among American men. The androgen receptor (AR) is vital for prostate cancer progression. Abiraterone acetate (AA) prolongs survival in castration-resistant prostate cancer (CRPC) by blocking CYP17A1, an enzyme required for androgen synthesis, but resistance invariably occurs. We hypothesize that abiraterone (abi) is endogenously converted by the enzyme 3β-hydroxysteroid dehydrogenase/isomerase (3βHSD) to a novel metabolite delta-4-abiraterone (D4A). We developed a liquid chromatography/tandem mass spectrometry (LC-MS/MS) method to analyze abi and its metabolite. Analysis of serum from CRPC patients treated with AA showed that abi is converted to the novel metabolite D4A.

Tuesday @ 12:10 PM in Catalina

**Right Target – Right Patient: Metabolomics Analysis Driving Pharmaceutical Development**

*Vladimir Tolstikov - BERG* (vladimir.tolstikov@berghealth.com)

- Recent advances in mass spectrometry technologies facilitated emerging Omics platforms capable translating biological output into therapeutic candidates. Metabolomics demonstrated tremendous promise in delivering quantitative information on differences in metabolism associated with disease onset/progression and pharmaceutical intervention. At BERG, we have implemented an industrial level high throughput metabolomics platform providing both high quality and depth of information allowing for reliable and broadest capture of the metabolome for the pre-clinical and clinical matrixes analyzed. Platform description and highlights of the BERG’s innovative approach for pharmaceutical development using in-depth patient stratification approaches as well as biology based drugs will be discussed.
MASS-FIX: A Comprehensive Methodology for Assessment of M-proteins Using Nanobody-Enrichment Coupled to MALDI-TOF Mass Spectrometry

John Mills - Mayo Clinic (mills.john2@mayo.edu) -- *Young Investigator Grantee*

* For 50 years electrophoretic separation of serum and urine proteins has played a central role in diagnosing and monitoring of plasma cell disorders. Despite limitations in resolution, sensitivity and the necessity for adjunct methods, protein gel electrophoresis and immunofixation electrophoresis remain front-line tests. A mass spectrometry (MS)-based assay was designed to be automatable, simple, cost-saving, sensitive and applicable to the variety of M-proteins encountered clinically. This assay, MASS-FIX, utilizes the unique molecular mass signatures of the different heavy chain and light chain isotypes in combination with nanobody-immunoenrichment to generate information-rich spectra from which M-proteins can be identified, isotyped, and quantitated. In this study we compared the performance of MASS-FIX to current gel-based electrophoresis assays.

How to Avoid a Bone Marrow Biopsy when Monitoring Minimum Residual Disease in Multiple Myeloma: Hope for the Future!

H. Robert Bergen, III - Mayo Clinic (bergen.bob@mayo.edu)

* Therapeutic effectiveness in multiple myeloma (MM) currently requires monitoring the relevant myeloma cells in a bone marrow sample. Because these plasma cell clones are producing a clonal antibody we sought to identify the antibody the clone was producing directly. Utilizing blood plasma where the M-protein is >0.8g/dL we have been able to identify unique tryptic peptides corresponding to immunoglobulin light chain variable regions belonging to each patients clone. Subsequent blood samples are utilized to measure MRD and the target peptide corresponding to each patients clone is monitored.

Mass Spectrometry Quantification of Personalized Biomarkers for Multiple Myeloma

Melissa Hoffman - Moffitt Cancer Center/University of South Florida (Melissa.Martinez@moffitt.org) -- *Young Investigator Grantee*

* Multiple Myeloma, an incurable disease with poor patient outcomes, is characterized by clonal expansion of the plasma cells in the bone marrow, which secrete a monoclonal immunoglobulin. This study utilizes a proteogenomics approach to develop individualized, peptide-based mass spectrometry assays to quantify each patient’s disease-specific biomarker. Personalized LC-MRM assays developed for variable region peptides using de novo RNA sequencing have shown a substantial increase in sensitivity compared to clinical methods. The increase in sensitivity improves minimal residual disease detection, which could improve patient outcomes.
Tuesday @ 11:30 AM in Pasadena

Automated Anatomical Atlas-assisted Interpretation of Differentially Expressed Proteins in Imaging Mass Spectrometry

Nico Verbeeck - Delft University of Technology (n.verbeeck@tudelft.nl)

* In recent years, imaging mass spectrometry (IMS) has gained increasing interest as a biomolecular screening tool, capable of detecting deviations in protein content between multiple tissue sections. In this work we aid the differential analysis of IMS data collected from healthy and diseased mouse brain tissue, by linking these data to an anatomical atlas. Differential protein signatures between the tissues are extracted using multivariate analysis techniques, and are then automatically interpreted in terms of anatomical structures using the Allen Mouse Brain Atlas. The automated interpretation of these inter-experiment differences can greatly accelerate differential exploration of IMS data sets by avoiding the time- and resource-intensive step of manually interpreting differential patterns using anatomical terms.

Tuesday @ 11:50 AM in Pasadena

Matrix-free Imaging of Metabolites and Lipids in Tissues and Bacterial Colonies by LAESI and NAPA Mass Spectrometry

Akos Vertes - George Washington University (vertes@gwu.edu)

* Spatial distributions of metabolites and lipids in biological tissues have been studied for decades by matrix-assisted laser desorption ionization mass spectrometry and secondary ion mass spectrometry. Despite the success of these techniques characterized by high mass capabilities and excellent spatial resolution, respectively, new ionization sources are being sought to provide better quantitation and fewer spectral interferences in the low mass region. Laser ablation electrospray ionization (LAESI) enables the two- and three-dimensional molecular imaging of tissues and bacterial colonies under ambient conditions. Thin tissue sections and subcellular structures (e.g., lamellipodia) on silicon nanopost array (NAPA) platforms are analyzed and imaged by laser desorption ionization mass spectrometry.

Tuesday @ 12:10 PM in Pasadena

Next-generation MALDI-IMS Capabilities for Ultra-high Throughput and Mass Resolution Protein Imaging

Jeffrey Spraggins - Vanderbilt University (jeff.spraggins@vanderbilt.edu)

* MALDI imaging mass spectrometry is a highly sensitive and selective tool used to visualize biomolecules in tissue. However, imaging of proteins remains a difficult task relative to lipids and metabolites. High-resolution protein imaging experiments have been limited by both sensitivity and throughput. Identification strategies have been restricted by insufficient mass accuracy to confidently link IMS to proteomics data. Here, we demonstrate next-generation imaging capabilities using MALDI-IMS. FTICR IMS provides unprecedented mass resolving power and accuracy for proteins up to ~18kDa, enabling identification based on correlation with LC-MS/MS proteomics data. High-speed MALDI-TOF platforms enable protein images to be collected at rates >20 px/s, facilitating new applications that require large number of pixels.
Tuesday @ 11:30 AM in Sierra

тDrug Stimulated Endocrinopathy: Impact of Opiates on Free Hormone Concentrations

Julie Ray - ARUP Laboratories (julie.ray@aruplab.com)

* Chronic use of opiates leads to adrenal and pituitary dysfunction and altered sexual function. Positivity of the drugs hydrocodone, oxycodone, morphine, methadone and gabapentin in 100 residual samples from adult men and women were evaluated for association with endocrine function. Concentrations of free testosterone, free estradiol, free thyroxine, free cortisol, triiodothyronine and reverse triiodothyronine in blood measured by LC-MS/MS methods were significantly impacted by the presence of these opiates. A gender based difference in metabolism of certain drugs was also noticed. Given the lack of clinical information regarding changes in levels of free hormones in opiate users, this could be important in determining the association of painkiller treatments with endocrine disorders.

Tuesday @ 11:50 AM in Sierra

тAre We Getting What We Paid for with a 13C-labeled Internal Standard?

Zlatuse Clark - ARUP Laboratories (zlatuse.d.clark@aruplab.com)

* 13C-labeled analogs are generally considered superior internal standards (IS) to deuterated analogs. Recently, we replaced a commercially available d5-IS in our dilute-and-shoot based method for urinary 5-hydroxyindoleacetic acid (HIAA) with a custom-synthesized HIAA-13C6 IS. How much has this change improved the quality of the assay? While HIAA-d5 necessitated a quadratic curve fit, HIAA-13C6 facilitated a highly linear calibration response, increasing method robustness. Method comparison showed a very good agreement between the HIAA-d5 and HIAA-13C6 based methods. A post-column infusion study of the 1.7% specimens with concentration discrepancies >±20% revealed discrepancies in quantitation due to differential signal suppression. Signal suppression simulation by post-column infusion of increasing concentrations of caffeine showed that HIAA-13C6 allows for more consistent quantitation.

Tuesday @ 12:10 PM in Sierra

тAnalysis of Aldosterone/plasma Renin Activity in a Single Method by Liquid Chromatography-tandem Mass Spectrometry (LC-MS/MS)

Dennis Orton - University of Calgary (dennis.orton@cls.ab.ca)

* The ratio of aldosterone to plasma renin activity (PRA) is used to help diagnose hyperaldosteronism (Conn's syndrome). This study presents a novel combined LC-MS/MS method for determination of the aldosterone/PRA ratio. PRA is measured following the formation of the product angiotensin I (angI) over time. Following solid phase extraction, aldosterone and angI were separated on a reversed phase column using both a methanol and pH gradient. The pH gradient is required to promote ionization of each analyte in positive (angI) and negative (aldosterone) modes. Combined analysis of aldosterone and PRA by LC-MS/MS provides an improved workflow in the clinical laboratory.
New Method Validation of a Broad Spectrum Drug Screen Using a High Resolution Time-Of-Flight Mass Spectrometer in the Clinical Toxicology Laboratory

Imir Metushi - UC San Diego Health (imetushi@ucsd.edu) -- *Young Investigator Grantee*

Urine drug screening is among the most widely used procedures in clinical toxicology laboratories. Recently, high resolution mass spectrometry (HRMS) such as time of flight-mass spectrometry (TOF-MS) has been proposed as an alternative for non-targeted drug screening. This session will discuss the applications of time-of-flight high resolution mass spectrometry (TOF-HRMS) in toxicology during drug testing and illustrates the approach that our institution has taken in validating a TOF-HRMS method for urine drug screening.

New Library Search Algorithm Improves Identification of Drugs in Urine by LC-QqTOF

Jennifer Colby - Vanderbilt University (jennifer.colby@vanderbilt.edu) -- *Young Investigator Grantee*

Library searching encompasses the computerized identification of compounds based on the similarity between an acquired mass spectrum and a spectrum found in a database. Library searching using commercially available algorithms and spectral libraries is a common practice in laboratories that use GC-MS, but it is also applicable to systems that collect product ion spectra, like liquid chromatography quadrupole time of flight mass analyzers (LC-QqTOF). We compared the ability of three library searching algorithms to match collected spectra against a spectral database, using 41 patient urine samples which were analyzed by LC-QqTOF. Our results indicate that an optimized library search algorithm can improve the efficiency of compound detection and reduce the manual review of putative matches.

High Resolution Mass Spectrometry for Suspect Screening of Novel Psychoactive Substances: Is It a Viable Solution for Clinical Laboratories?

Kara Lynch - University of California, San Francisco (kara.lynch@ucsf.edu)

The use of LC-HRMS is becoming more common for small molecules identification in a variety of analytical fields. With LC-HRMS, data acquisition is untargeted and the resulting data can be analyzed using targeted, suspect, and untargeted data analysis. The continued use of novel psychoactive substances (NPS) presents a significant analytical challenge for toxicology laboratories trying to keep their analytical methods up-to-date. Purchasing all possible NPS analytical standards is not practical for most laboratories. The objective of this study was to evaluate the utility of suspect screening with and without library matching to identify emerging amphetamine-type NPS in our patient population.
Tuesday @ 4:00 PM in Mojave Learning Center

**Basic Principles of Data Review**

*Robert Fitzgerald* - UCSD (rfitzgerald@ucsd.edu)

Data review is an essential component of reporting any laboratory data. In the case of clinical mass spectrometry there are key components to this review that can be performed manually or by various automated approaches. Before automating data review it is essential that the basic principles of data review are understood. In the first session of this track we will discuss the basics of data review to set the stage for two approaches using automation to simplify this process. Examples of acceptable and unacceptable batches of data will be presented.

Tuesday @ 4:20 PM in Mojave Learning Center

**Data Review Using Vendor Software and Rules Systems**

*Krista Pratico* - UCSD Center for Advanced Laboratory Medicine (kpratico@ucsd.edu)

Mass spectral data review and result entry can be a time consuming and sometimes erroneous process leading to unfavorable patient outcomes. While commercial data analysis software is available, vendor software can be used to automate some aspects of data review and calculate meta-data to generate flagging for outliers needing additional review. We describe the development and validation of semi-automated workflows using vendor software in conjunction with an LIS-based rules engine. An alternative approach using a rules engine integrated with middleware will also be described. Both yield significant productivity and decreased turn-around-time in high to moderate volume LC-MS laboratories.

Tuesday @ 4:40 PM in Mojave Learning Center

**Automated Data Review Using Homebrew Software**

*Sheng-Ying Lo* - University of Washington (mslo@uw.edu)

The analysis of multiplexed LC-MS/MS data can be a complicated task. This session will describe the experience of a single institution with in-house software to analyze mass spectrometry data containing 828 data points per patient sample. Utilization of this software has reduced the time required for data analysis and has improved the consistency of the QA procedures as they are applied from day-to-day in our assay that measures 23 opioids and opioid metabolites in urine.
Tuesday @ 4:00 PM in Catalina
Metal Oxide Laser Ionization (MOLI) MS for Identification of Bacteria Using Fatty Acid Profiling
Kent Voorhees - Colorado School of Mines (kvtv@comcast.net)

- Recently, matrix-assisted laser desorption ionization MS (MALDI MS) instruments were utilized with metal oxides as a matrix replacement and catalyst to cleave bacterial lipid extracts to their constituent fatty acids. Utilizing this novel approach designated metal oxide laser ionization (MOLI) MS, with CaO, NiO, and CeO2, fatty acids and lipid material from bacterial membrane lipids in the source of the MS were produced, resulting in profiles that were used to identify microorganisms. The data from diverse bacterial phenotypes have shown that MOLI MS is a strain-level detection system providing leave-one-out cross validation results greater than 98 percent. Organism classification results from several metal oxides will be presented.

Tuesday @ 4:20 PM in Catalina
Strain-level Bacterial Identification by CeO2-catalyzed MALDI-TOF MS Fatty Acid Analysis and Comparison to Commercial Protein-based Methods
Chris Cox - Colorado School of Mines (crcox@mines.edu) -- *Young Investigator Grantee*

- MALDI-TOF MS has emerged as a rapid approach for clinical bacterial identification. Current protein-based methods, while widely accepted, fall short when differentiating closely related phylotypes. To address this, we employed in situ CeO2-catalyzed lipid fragmentation into taxonomically viable fatty acids using the energy inherent to the MALDI laser as an alternative to protein profiling. We observed consistent strain-level ID of a diverse collection of Acinetobacter, Enterobacteriaceae, and Listeria, which were difficult or impossible to differentiate with the Bruker Biotyper. In comparison, protein profiling resulted in significantly lower accuracy and was unable to ID any bacteria at the strain level.

Tuesday @ 4:40 PM in Catalina
Using Rapid Evaporative Ionisation Mass Spectrometry (REIMS) to Assign Taxonomic Classifications to Microbial Isolates and Mixed Communities
Simon Cameron - Imperial College, London (s.cameron@imperial.ac.uk) -- *Young Investigator Grantee*

- Mass spectrometry has revolutionised clinical microbiology laboratories’ work flows, and decreased diagnosis times. Rapid evaporative ionisation mass spectrometry (REIMS) has previously been show to allow the differentiation of fungi and bacterial species based upon their lipidomic profiles. Work is currently underway to construct a REIMS mass spectra library of approximately 50,000 isolates from 4,000 species, using a high-throughput, semi-automated platform incorporating colony imaging and picking. This mass spectra library will be utilised in the identification of microbial isolates without the preparative steps required for MALDI-ToF. Furthermore, the effectiveness of using REIMS analysis to identify microbes from multiple species samples will be evaluated. This will be completed without the prior isolation of pure microbial cultures, thereby significantly reducing time to diagnosis.
Tuesday @ 4:00 PM in Madera
**Longitudinal Measurement of Protein Biomarkers in Healthy Individuals and Elite Athletes**
*Leigh Anderson - SISCAPA Assay Technologies* (leighanderson@siscapa.com)

- Precise, longitudinal measurement of protein biomarkers in dried-blood-spots (DBS) is an attractive option for providing preventative, personalized medicine at reasonable cost. Here we present the results of longitudinal measurement of 22 proteins in DBS samples collected from ‘healthy’ individuals and elite athletes. Unique ‘protein-fingerprints’ were defined for each individual to monitor various body functions. Of particular interest were a panel of proteins used to measure the extent of muscle damage in athletes as a result of training/competition. We are currently assessing the effectiveness of such personalized protein measurements in preventing severe muscle damage as a result of ‘over-training’.

Tuesday @ 4:20 PM in Madera
**Quantitation of Albumin and Creatinine in Urine by MALDI-TOF Mass Spectrometry**
*Stephen Hattan - SimulTof Systems* (stephen.hattan@simultof.com)

- “Albuminuria” is elevated levels of serum albumin (SA) in urine (U) and can indicate kidney malfunction / disease. We demonstrated a novel means for quantifying albumin directly or in comparison to creatinine (C) in urine by MALDI-TOF mass spectrometry. Standard addition of albumin and deuterated creatinine (d3) into control urine produced a linear and quantitative response (R² = 0.99 and 0.98) used to quantify both in patient samples across the relevant ranges of 5 – 500 mg/L C (SA/U) and 300 – 4000 mg/L (C/U) with CV < 10%. This MS-based method represents a simple, fast, attractive alternative to currently clinical methods.

Tuesday @ 4:40 PM in Madera
**Apolipoprotein C-III Proteoforms as Biomarkers for Changes in Lipid Metabolism**
*Olgica Trenchevska - Arizona State University* (olgica.trenchevska@asu.edu)

- Proteins can exist in multiple proteoforms in vivo in different physiological and pathological states. In this work, we addressed the potential of utilizing proteoforms as clinical markers, by exploring the association between apolipoprotein C-III (apoC-III) proteoforms and lipid metabolism. We used mass spectrometric immunoassay to perform cross-sectional and longitudinal characterization of apoC-III proteoforms in obese adolescents, and patients with impaired glucose tolerance and type 2 diabetes. We found strong inverse and independent associations between the relative amount of disialylated apoC-III and plasma triglycerides concentrations in all three cohorts. Other measures, such as cholesterol distribution, also correlated with apoC-III proteoforms.
Tuesday @ 4:00 PM in Pasadena

**Lipid Imaging for Cancer Diagnosis by Ambient Mass Spectrometry**

*Livio S. Eberlin - The University of Texas at Austin* (liviase@utexas.edu)

There is a clinical need for new technologies that would enable rapid disease diagnosis based on diagnostic molecular signatures. Ambient ionization mass spectrometry has revolutionized the means by which molecular information can be obtained from tissue samples in real time and with minimal sample pretreatment. The latest developments in ambient ionization techniques applied to clinical research suggest that ambient ionization mass spectrometry will soon become a routine medical tool for tissue diagnosis. This talk will cover the main developments in ambient ionization techniques applied to lipid imaging and tissue analysis, with focus on the use of desorption electrospray ionization mass spectrometry for cancer diagnosis. Recent approaches to incorporate this technology for routine, clinical use in the treatment and management of cancer patients will be discussed.

Tuesday @ 4:20 PM in Pasadena

**Imaging Mass Spectrometry and Metabolomics in Parkinson’s Disease**

*Timothy Garrett - University of Florida* (tgarrett@ufl.edu)

Imaging mass spectrometry (IMS) enables the direct analysis of compounds from tissue and the technique produces images that correlate to the distribution in tissue. When connected to metabolomics, this technique can provide a unique perspective of metabolism. Parkinson’s Disease (PD) is a movement disorder involving the loss of dopaminergic neurons as well as degeneration of multiple brain circuits. Deep brain stimulation (DBS) is a surgical treatment utilizing electrical stimulation to target a specific brain nucleus. Despite the effectiveness of DBS, little is known about the mechanism. We have utilized IMS and LC-HRMS metabolomics to evaluate the changes in small molecules in relation to PD and the potential changes to small molecules following DBS.

Tuesday @ 4:40 PM in Pasadena

**IR-MALDESI: An Innovative Approach to Molecular Microscopy**

*David Muddiman - North Carolina State University* (dcmuddim@ncsu.edu)

This presentation will detail our efforts at the fundamental development and application of a novel mass spectrometry imaging technique called IR-MALDESI. This will be demonstrated for both targeted, quantitative studies as well as untargeted analyses.
Tuesday @ 4:00 PM in Sierra

A Case Study in the Development and Implementation of a Calculated Free Testosterone Assay for the Clinical Laboratory

Benjamin Beppler - TriCore Reference Laboratories (benjamin.beppler@tricore.org)

* Most clinical laboratories opt to calculate free testosterone based on direct measurements of total testosterone and appropriate binding proteins. The reliability of this calculation, however, is complicated by a variety of factors. In this talk, we demonstrate the effect of choosing different calculations, total testosterone methods, and Sex Hormone Binding Globulin (SHGB) assays, as well as the importance to compare calculated results against a reference method using the most appropriate regression analysis. Options regarding choosing appropriate reference ranges will also be discussed.

Tuesday @ 4:20 PM in Sierra

Evaluation of Matrices for the Development of Calibrators in Therapeutic Monitoring of Hormones, Drugs and Biomarkers: Testosterone Case Study

Uma Sreenivasan - Cerilliant Corporation (uma_sreenivasan@cerilliant.com)

* Accuracy based calibrators are critical for accurate quantitation of endogenous hormones, biomarkers and drugs in clinical diagnostics. Endogenous levels of analytes or impurities in serum and stripped sera, can interfere with accuracy of low level calibrators. Stripped and synthetic matrices must also demonstrate commutability and performance equivalent to the endogenous matrix. High sensitivity LC-MS/MS and QTof procedures were developed for matrix screening and comparison. Synthetic matrices and stripped human sera were screened for use as calibration matrix for the quantitation of Testosterone. Critical performance requirements related to endogenous and extraneous interferences were identified and control strategies developed.

Tuesday @ 4:40 PM in Sierra

Simultaneous Measurement of Testosterone and Estradiol in Serum by LC-MS/MS without Derivatization

Dean Carlow - Memorial Sloan Kettering Cancer Center (carlowd@mskcc.org)

* Our objective was to develop a very sensitive LC-MS/MS assay for both testosterone and estradiol in serum in a single analysis without the need for chemical derivatization. Serum samples were prepared by the addition of deuterated internal standards followed by a liquid-liquid extraction and LC-MS/MS in both positive and negative ion modes. The assay was very sensitive, had wide analytical measurement ranges and was precise. The accuracy was assessed by comparison with established LC-MS/MS assays, recovery studies, and comparison with several different reference materials. We have successfully developed an accurate and highly sensitive assay to simultaneously measure testosterone and estradiol levels in serum.
Tuesday @ 4:00 PM in SmokeTree  
Investigation of a Large Pain Profile from Fingerstick Capillary Blood  
**Jeffrey Enders** - Ameritox, Ltd. (jeffrey.enders@ameritox.com)

- Blood-based analysis has historically been the standard of forensic drug testing. Factors which have previously prevented blood from being the matrix of choice in pain management drug analysis, have recently been attenuated by a new sampling device which is able to collect a specific volume of blood through a fingerstick, thus negating the necessity of a phlebotomist. Commonly, fingerstick blood has been associated with various endogenous-based assays, such as glucose, hemoglobin, and genetic testing. However, in this work it will be shown that capillary blood from a fingerstick can be used to assess a patient’s exogenous compound profile.

Tuesday @ 4:20 PM in SmokeTree  
Specifically Opioids: The Importance of LC in LC-MS/MS in Opioid Therapy Monitoring and Compliance Testing  
**Matt Salske** - Essential Testing (msalske@etlab.org)

- Mass spectrometry (MS) is a useful tool in the evaluation of patient compliance in opioid therapy. However, MS detection, in the absence of complimentary techniques such as liquid chromatography, can be fooled. This presentation will elucidate sources of selectivity challenges related to opioid analysis as a function of both biological and mass spectrometric generated interferences, demonstrating the need for an additional dimension of selectivity.

Tuesday @ 4:40 PM in SmokeTree  
**Joseph Rudolf** - Massachusetts General Hospital (jrudolf1@partners.org) -- *Young Investigator Grantee*

- Guidelines for workplace screening and confirmation of semi-synthetic opiates in oral fluid have been proposed by SAMHSA. We evaluate the proposed guidelines for oxycodone/oxymorphone and hydrocodone/hydromorphone using results from our institution’s toxicology service (5406 samples). The proposed confirmatory cutoff of 15 ng/ml identifies a majority of our positive cases for oxycodone and hydrocodone. Simulated immunoassay class cross-reactivity did not substantially increase the number of cases requiring confirmation (221 to 223 for oxycodone, 27 to 32 for hydrocodone). Lowering the confirmatory cutoff to 4 ng/ml does increase the number of positive cases (256 to 310 for oxycodone, 35 to 49 for hydrocodone).
Wednesday @ 11:30 AM in Mojave Learning Center
**A Regulatory Review of Quality Assurance Monitoring for LC-MS**
* Kara Lynch - University of California, San Francisco (kara.lynch@ucsf.edu)

Until recently, there existed minimal regulatory guidance on the use of LC-MS for clinical diagnostics. The Clinical and Laboratory Standards Institute (CLSI) has now presented a standardized approach for LC-MS assay development, verification and quality assurance monitoring in its new guidance document, CLSI C62-A. This talk will review the recommendations presented in this document for quality assurance monitoring of LC-MS quantitative assays. Consensus recommendations set forth by other regulatory agencies will also be reviewed and compared.

Wednesday @ 11:50 AM in Mojave Learning Center
**Part 1: Effective Utilization of Quality Assurance Metrics in LC-MS/MS: Practical Examples**
* Lorin Bachmann - Virginia Commonwealth University (lorin.bachmann@vcuhealth.org)

Current laboratory practice guidelines outline metrics that should be monitored as part of quality assurance (QA) programs for quantitative LC-MS/MS. However, few resources are available to instruct laboratorians on specific steps need to design and establish a value-added QA program. In this session, practical examples and step-by-step instructions will be provided to demonstrate how to effectively and efficiently select QA parameters, establish QA acceptability criteria, monitor QA data and utilize QA metrics to critically assess performance of LC-MS/MS methods.

Wednesday @ 12:10 PM in Mojave Learning Center
**Part 2: Effective Utilization of Quality Assurance Metrics in LC-MS/MS: Practical Examples**
* Lorin Bachmann - Virginia Commonwealth University (lorin.bachmann@vcuhealth.org)

Current laboratory practice guidelines outline metrics that should be monitored as part of quality assurance (QA) programs for quantitative LC-MS/MS. However, few resources are available to instruct laboratorians on specific steps need to design and establish a value-added QA program. In this session, practical examples and step-by-step instructions will be provided to demonstrate how to effectively and efficiently select QA parameters, establish QA acceptability criteria, monitor QA data and utilize QA metrics to critically assess performance of LC-MS/MS methods.
Wednesday @ 11:30 AM in Catalina
Tandem Mass Spectrometry for Newborn Screening and Diagnosis of Lysosomal Storage Diseases
Michael Gelb - Univ. of Washington (gelb@chem.washington.edu)
• Our lab has developed all of the mass spectrometry methods being used in newborn screening of lysosomal storage diseases worldwide. We are continuing to develop these assays and to carry out large scale pilot studies to test the feasibility of newborn screening for lysosomal storage diseases. Mass spectrometry has emerged as the most broadly used and reliable newborn screening method for lysosomal storage diseases.

Wednesday @ 11:50 AM in Catalina
Examination of S-adenosylmethionine/S-adenosylhomocysteine and DNA Methylation in Mouse Models of Cystathionine β-synthase Deficiency
Yin-Ming Kuo - Fox Chase Cancer Center (yin-ming.kuo@fccc.edu) -- *Young Investigator Grantee*
• Cystathionine β-synthase (CBS) deficiency is an inborn error of metabolism characterized by high levels of serum total homocysteine. To better understand how hyperhomocysteine (alteration of one-carbon metabolism) affects pathogenesis, we utilized LC-MS/MS methods to examine the levels of S-adenosylhomocysteine (AdoHcy), S-adenosylmethionine (AdoMet), and the percentage of 5-methyldeoxycytidine in tissues from two mouse models of CBS deficiency: Tg-hCBS Cbs-/-, and Eµ-myc mice. Our results reveal that CBS deficiency results in elevated AdoHcy levels and reduced AdoMet/AdoHcy ratio in liver, kidney, and tumor tissues. However, there is no clear evidence linking this change to further epigenetic modulation and biological effect.

Wednesday @ 12:10 PM in Catalina
Decompensation Events in Maple Syrup Urine Disease (MSUD): The Impact of Mass Spectrometry on Acute Management
Andy De Souza - BC Children's Hospital (andy.desouza@cw.bc.ca)
• The Newborn Screening Program at BC Children’s Hospital has diagnosed and confirmed 3 cases of MSUD since 2010. When stable, these patients are routinely monitored as outpatients, with plasma amino acid samples analyzed by the Biochemical Genetics Laboratory (BGL). BGL implemented TMS for plasma amino acid analysis in Spring 2014, switching from the widely used method of IEC coupled with post-column ninhydrin derivitization, a change that has improved testing capacity, reduced average turn-around-times, and streamlined laboratory workflows. In this presentation, we will demonstrate the impact that this method change has had on patient quality of care for acute admissions, using a case of an MSUD patient during an extended hospital stay for an acute decompensation event. Response times for “STAT” testing and the impact this had on immediate clinical management will be presented.
Wednesday @ 11:30 AM in Madera

**Mass Spectrometry Analysis of CNS Specific Oligoclonal Immunoglobulins**

*Patrick Vanderboom - Mayo Clinic* (vanderboom.patrick@mayo.edu)

- Isoelectric focusing followed by IgG specific immunoblotting is used to detect immunoglobulins specific to the CNS compartment (oligoclonal banding) and is routinely used as part of the diagnostic criteria for multiple sclerosis. The current isoelectric focusing based reference method is labor intensive and relies on a subjective interpretation of IgG bands from paired CSF and serum. Here, we demonstrate the advantages of a recently developed high throughput mass spectrometry based method which leverages the power of accurate molecular mass to detect and characterize oligoclonal immunoglobulins in CSF.

Wednesday @ 11:50 AM in Madera

**Resolving Discrepancies in Immunonephelometric Total IgG and IgG Subclass Measurements with Mass Spectrometry**

*Andre Mattman - University of British Columbia* (amattman@providencehealth.bc.ca)

- IgG subclasses are measured clinically to diagnose IgG4 related disease. In some patient samples, the sum of the immunonephelometric quantification of the individual subclasses (sum (IgGs)) is much greater than the immunonephelometric total IgG test. 84 samples with a range of IgG4 values were retrieved. In the IG4RD cohort, the sum (IgGs), when measured by immunonephelometry, was greater than total IgG as measured by any of three methods (immunonephelometry, electrophoresis or LC-MS/MS). This bias between sum (IgGs) and total IgG was predicted by IgG4 levels and was absent when all measurements were by LC-MS/MS.

Wednesday @ 12:10 PM in Madera

**Peptide Selection for Amyloidosis Diagnosis and Typing**

*Han-Yin Yang - University of Washington* (hyyang@uw.edu) -- *Young Investigator Grantee*

- Laser-capture microdissection (LMD) used in conjunction with tandem mass spectrometry (MS/MS) has been a superior alternative to the previously applied immunohistochemistry assay. However, there are several aspects of current approach can be reconsidered. Here, we applied a systematic sampling MS/MS strategy to unbiased quantify amyloidosis peptides in different samples. We aim to find a subset of amyloid relate peptides that has best discriminate power for amyloidosis diagnosis and sub-typing using FFPE sample. Preliminary results show that we could successfully type and distinguish amyloidosis and normal cases base on the observed intensities of selected peptides.
Integrating Mass Spectrometry with Other Imaging Technologies: Improving Biological Insight Through Multi-modal Image Fusion

**Raf Van de Plas - Delft University of Technology (raf.vandeplas@tudelft.nl)**

Medical studies increasingly employ a multitude of different imaging technologies to answer a specific biological question. A growing number of such multi-modal imaging studies include Imaging Mass Spectrometry (IMS) as one of these modalities. Although different modalities are routinely registered and overlaid to generate a single display, true integration of data across technologies is largely left to human interpretation, resulting in a significant underutilization of the potential of multi-modal measurements. This talk gives an overview of our recent work on the integration or ‘fusion’ of IMS with measurements from other imaging modalities, and demonstrates the potential of data-driven image fusion for IMS through several predictive applications.

Statistical Methods for Mass Spectrometry-based Imaging

**Olga Vitek - Northeastern University (o.vitek@neu.edu)**

Statistical methods are key for detecting signals (e.g., caused by an intervention or a disease) in presence of variation and uncertainty. This is particularly important for mass spectrometry-based imaging, where signals are obscured by variation between different biological replicates, the spatial variation within images of a same biological replicate, and the technical variation due to sample handling and spectral acquisition. Moreover, as spatial and mass resolution increase, the experiments become more prone to generating spurious associations, and to amplifying bias and confounding. This talk will discuss the importance of statistical inference when designing and analyzing mass spectrometry-based imaging experiments, as well as statistical methods and open-source software designed to facilitate the statistical inference tasks.

De novo Discovery of Phenotypic Intra-tumor Heterogeneity Using Imaging Mass Spectrometry

**Benjamin Balluff - Maastricht University (b.balluff@maastrichtuniversity.nl)**

A so far unresolved factor influencing the evolution of cancer and the clinical course of patients is intra-tumor heterogeneity. In this presentation a pipeline using imaging mass spectrometry will be presented for the systematic de novo discovery of clinically detrimental tumor subpopulations. Therefore, spatially-resolved mass spectra are clustered for revealing molecularly distinct regions with the tumor. The simultaneous segmentation of many samples and investigation if the presence of certain clusters is statistically associated with the clinical outcome of the patients, allows identifying phenotypic tumor subpopulations which –after dissection– can be further molecularly characterized by other omics approaches.
Application of MUSCLE Software as an Automated Approach to LC-MS/MS Method Development for the Analysis of Multiple Vitamin D Metabolites

Carl Jenkinson - Metabolism and Systems Research, University of Birmingham (C.Jenkinson@bham.ac.uk) -- *Young Investigator Grantee*

- Increased demand has been placed on clinical laboratories to develop and run rapid liquid chromatography-tandem mass-spectrometry (LC-MS/MS) methods to accurately quantify multiple analytes of interest. Manual method development can be time consuming and challenging, particularly with multiple metabolites. This study utilises a software platform, MUSCLE, for automated method development of multiple vitamin D metabolites, comparing the optimised parameters with a manually developed method. The optimised MUSCLE method reduced the overall method run time from 9 minutes to 6.5 minutes although mass spectrometry transitions did not alter significantly with either method. This study illustrates the use of MUSCLE for clinical laboratories for reducing labour and time for developing LC-MS/MS methods.

Alternative Approaches for Producing Micro Samples of Dried Plasma for Automated LC/MS/MS Determination of Opioid Drugs

Jack Henion - Q2 Solutions (henionj@advion.com)

- Previously we have reported on the development of a homemade dried plasma spot (DPS) card which was used for collection, transport, storage and automated LC/MS/MS bioanalysis for the ADHD drug, quanfacine. This DPS card provided acceptable results for normal hematocrit blood, but did not provide acceptable precision and accuracy results for the extremes of hematocrit (30% and 60%). This presentation will describe a recent alternative approach which provides dried plasma without the need for centrifugation. The ‘filtration’ of red blood cells is accomplished with a filtration mechanism and the workflow is more amenable to a high-throughput laboratory.

Design of Experiments for Optimization of Quantitative LC-MS/MS Clinical Diagnostic Methods

Margret Thorsteinsdottir - University of Iceland (margreth@hi.is) -- *Young Investigator Grantee*

- Tandem mass spectrometry coupled to liquid chromatography (LC-MS/MS) is an excellent analytical platform for quantification of biomarkers in biological matrices. Method development consists of several integrated steps involving many experimental factors which need to be simultaneously optimized to obtain maximum selectivity and sensitivity at minimum retention time. This work will illustrate that method optimization can become much more efficient by utilizing design of experiments (DoE). Examples will be given to illustrate how DoE works for optimization of LC-MS/MS clinical diagnostic methods using only a fraction of experiments that would be required by changing one-factor-at-time (OFAT) approach.
**Session 3 • Track 6 •
New Sample Types and Introduction Techniques for Drug Analysis**

**Wednesday @ 11:30 AM in SmokeTree**

**Session Chair: Russell Grant - LabCorp**

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**Wednesday @ 11:30 AM in SmokeTree**

**Analysis of 29 Drugs of Abuse in Exhaled Breath Using UHPLC-MS/MS**

*Shahid Ullah* - Karolinska Institute (shahid.ullah@ki.se) -- *Young Investigator Grantee*

* Drugs abusing is a serious public health concern that affects almost every community in the world. Using these substances may lead to a severe mental and physical disorder and may endanger human life. In this study, a mass spectrometric method has been validated to analyze 29 psychoactive drugs in exhaled breath. Approximately 30L of exhaled breath was sampled to a polymer filter, extracted with methanol and analyzed by LC-MS/MS. Method detection limits were ≤ 10 pg/filter for most of the analytes and method recoveries were in the range of 70 to 120% for all analytes.

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**Wednesday @ 11:50 AM in SmokeTree**

**Advances in the Development of Touch Spray Mass Spectrometry with Medical Swabs for Drug Detection in Oral Fluid**

*Valentina Pirro* - Purdue University (vpirro@purdue.edu)

* Touch spray (TS) with medical swabs was recently developed as an ambient ionization technique for direct oral fluid analysis in point-of-care clinical-toxicological applications. We present recent advances to this methodology for the detection of over 20 common drugs and pharmaceuticals in oral fluid. Fundamental aspects of ionization were explored including swab tip material and geometry, solvent flow rate, etc. Electric field simulations and recorded video of the ionization process allow further understanding of the ionization phenomenon. In addition to the detection of common drugs via targeted MSn, a data-independent MS/MS strategy using TS is presented as drug screening methodology.

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**Wednesday @ 12:10 PM in SmokeTree**

**Rapid Characterization of Drugs and Metabolites on Skin by Ambient Mass Spectrometry**

*Jentaie Shiea* - National Sun Yat-Sen University (jetea@mail.nsysu.edu.tw)

* TD-ESI/MS was employed to characterize caffeine, lamisil, acetaminophen, and plasticizers released on skin. The metal sampling probe has been designed in such a way that it is easily to collect samples directly from skin as well as mass spectrometric detection without any treatment. After the volunteers taking the drug for a period of time, the drug distribution throughout the whole body was studied. Taking lamisil, an anti-fungus drug, as an example; the ion signal of lamisil was found mostly on the upper body especially face. In addition, pharmacokinetic profile of a drug can be determined by analyzing the samples collected from skin with TD-ESI/MS. No blood withdrawing or urine collection is needed. The phthalates released on skin were studies to evaluate the level of an individual exposed to such environmental hormones.
• Session 4 • Track 1 •
Sleep Soundly at Night when Using LC-MSMS - Quality & Personnel
Wednesday @ 4:00 PM in Mojave Learning Center
Session Chair: Shannon Haymond - Northwestern University Feinberg School of Medicine

Wednesday @ 4:00 PM in Mojave Learning Center
Setting Up Your Mass Spectrometry (MS) Team for Success
Daniel Holmes - University of British Columbia (dtholmes@mail.ubc.ca)
* During MS method development we focus on metrics such as linear range, limit of quantitation, selectivity, accuracy, and precision. However we often fail to optimize factors equally important for good performance in the production phase (robustness, ease of use, etc), thus setting our teams up for failure. We will discuss attributes that make an SOP and all phases of an MS assay workflow scalable and user-friendly at launch and with increasing test volumes. Finally we will discuss personality traits and work habits of highly successful mass spectrometry operators and what we can do to recruit, mentor and retain them.

Wednesday @ 4:20 PM in Mojave Learning Center
Part 1: Tips and Tools for Training and Competency with Clinical LC-MS
Shannon Haymond - Northwestern University FSM (shaymond@luriechildrens.org)
* One of the key considerations and potential areas of apprehension for implementing liquid chromatography tandem mass spectrometry (LC-MS/MS) is staff training. The number of laboratory staff with exposure to LC or MS/MS is relatively limited, and even fewer have experience with clinical applications of LC-MS/MS. This session will introduce our approach for training staff and assessing competency, following current best practices. An interactive component will provide tools participants may apply to their own lab operation.

Wednesday @ 4:40 PM in Mojave Learning Center
Part 2: Tips and Tools for Training and Competency with Clinical LC-MS
Shannon Haymond - Northwestern University FSM (shaymond@luriechildrens.org)
* One of the key considerations and potential areas of apprehension for implementing liquid chromatography tandem mass spectrometry (LC-MS/MS) is staff training. The number of laboratory staff with exposure to LC or MS/MS is relatively limited, and even fewer have experience with clinical applications of LC-MS/MS. This session will introduce our approach for training staff and assessing competency, following current best practices. An interactive component will provide tools participants may apply to their own lab operation.
Comprehensive Metaproteomic Analyses of Urine in Cases of Urinary Tract Infection and Colonization/Absence of Bacteriuria  
Yanbao Yu - J. Craig Venter Institute (yayu@jcvi.org) -- *Young Investigator Grantee*

Non-invasively collected urine is a valuable source to clinical diagnosis and prognosis. However, most urinary proteomic studies reported to date worked with supernatant. The resulting sediment/pellet was often discarded as wastes. Urine sediments were recently found to be informative regarding urinary tract infections. In this study, we first used a metaproteomic approach to profile the human and microbial proteomes of the entire urine specimens. Second, we quantitatively analyzed the differences of the two urine fractions with label-free approach. Finally, we identified proteomic differences in both fractions in the context of identifications for uropathogens and commensal organisms and evidence of urothelial injury and hematuria.

Identification of Bacteria by MALDI by Matching to Translated DNA Databases  
Kenneth Parker - SimulTOF Systems (kenneth.parker@simultof.com)

Software has been written that enables bacterial identification starting from MALDI spectra of colony extracts by mapping directly against a database of mostly ribosomal protein sequences extracted from complete proteomes in public repositories. Every organism whose protein sequences have been deposited can potentially be identified using this approach, whether or not that organism has ever been grown in culture. Each of several thousand bacterial strains receives scores, together with tables listing identified protein sequences. The results for identifying certain Gammaproteobacteria and Firmicutes derived from ATCC collections will be shown. So far, most species included in the downloaded database that have been tested have been identified using this approach.

Targeted Metabolic Profiling for Qualitative and Quantitative Measurement of Bacterial Metabolites and their Response to Antibiotic Treatment  
Jiangjiang (Chris) Zhu - Miami University (zhuj6@miamioh.edu) -- *Young Investigator Grantee*

Here we demonstrated a study focused on the development and application of targeted metabolic profiling for detecting and monitoring the bacterial metabolic profile changes in response to antibiotics treatment. Hydrophilic interaction liquid chromatography (HILIC) - tandem mass spectrometry method was used for metabolic profiling. More than 100 targeted metabolites, include amino acids, fatty acids, purine metabolites, pyrimidine metabolites as well as carboxylic acids have been targeted for metabolic changes due to antibiotic treatment. Our results indicated that the metabolic profile after treatment of antibiotics could aid the differentiation of MSSA strains and MRSA strains, which can be potentially applied in clinical application for antibiotic resistance test.
Using a Stable Isotope-labeled Protein and Corresponding Set of Stable Isotope-labeled Peptides as Comprehensive Quality Controls for Bottom-up Proteomics

James Bollinger - University of Washington (jgb2@uw.edu) -- *Young Investigator Grantee*

- Liquid chromatography used in-line with tandem mass spectrometry (LC-MS/MS) has emerged as the dominant analytical platform for bottom-up proteomics. Described herein is a workflow that utilizes a stable isotope-labeled protein and accompanying set of differentially stable isotope-labeled peptides for the purpose of controlling the variation imparted during sample preparation and MS/MS analysis while simultaneously benchmarking tryptic digestion status and incorporating the indexed retention time (iRT) concept.

Is It Better to Be Lucky or Absolute in Protein Quantification?

Christopher Shuford - Laboratory Corporation of America (shuforc@labcorp.com)

- In order to overcome the shortcomings of peptide calibrators, many efforts have been made to use full-length proteins as calibration materials with the premise that conversion of a full-length protein calibrator into its signature peptide(s) will occur with the same efficacy as conversion of the endogenous protein to be measured. If this is universally true, then the accuracy of protein-calibrated assays would be independent of 1) the digestion conditions employed and 2) the signature peptide selected. In our efforts to quantify the endogenous protein biomarker, thyroglobulin, using full-length protein calibrators and internal standards we have observed this not to be the case – indicating full-length proteins calibrators do not universally provide absolute quantification.

Strategies for Improving Specificity and Sensitivity for Multiplexed Proteomic Assays in for High-Flow, Fast-Gradient LC-MS in the Clinical Laboratory

Timothy Collier - Cleveland HeartLab, Inc. (tcollier@clevelandheartlab.com)

- The potential for multiplexed proteomic assays is a key advantage of MS in the clinical laboratory. However, demands on throughput require rapid LC-MS, compressing analytical space and increasing chances for interference and suppression. Here, we describe the analytical challenges posed in the development of a high-flow, short-gradient, MRM method on a subset of the serum proteome, including the use of alternate enzymes and strategies to optimize sample preparation, the need to characterize analyte specific ion suppression, and contend with the possibility of nonspecific effects from co-eluting nominally isobaric species.
Wednesday @ 4:00 PM in Pasadena

Cell-by-cell Measurement of Metabolic Activity in the Early Developing Embryo

Peter Nemes - George Washington University (petern@gwu.edu) -- *Young Investigator Grantee*

- Knowledge of all molecules in embryonic cells raises a potential to holistically understand basic processes that orchestrate the development of the normal embryo. However, the complex three-dimensional and spatiotemporally evolving structure of the embryo poses significant analytical challenges in capturing molecular differences between cells using mass spectrometry, particularly at the level of metabolites that are complex and also dynamic. We describe here a microsampling approach to find metabolic differences between identified single cells in the 16-cell frog (Xenopus laevis) embryo. In combination with functional studies, we discover metabolites that are able to alter the developmental fate of embryonic cells.

Wednesday @ 4:20 PM in Pasadena

Molecular Diagnosis of Benign and Malignant Melanocytic Lesions Using Mass Spectrometry Imaging

Erin H. Seeley - Protea Biosciences, Inc. (erin.seeley@proteabio.com)

- Mass spectrometry imaging (MSI) is an emergent technology for the analysis of clinical samples. Here, we present an application of MSI to the molecular diagnosis of human melanocytic skin lesions. A training set of 25 benign nevi and 25 malignant melanomas were interrogated and used to create a genetic algorithm for classification. This algorithm was then validated in an independent set of lesions (sensitivity 97%, specificity 85%). Ongoing work is looking at the application of the algorithm to melanocytic lesions that fall in the histologic “gray area” as well as identification of the peptides that were part of the classifier.

Wednesday @ 4:40 PM in Pasadena

High Resolution Molecular Imaging: Revealing More Detail in Clinical Studies

Ron M.A. Heeren - Maastricht University, M4I (r.heeren@maastrichtuniversity.nl)

- A multimodal approach for molecular imaging for clinical studies is trending the field of imaging mass spectrometry. More and more researchers realize that a single technology provides only a subset of the molecular information needed to obtain an in depth understanding of a clinical problem. Multimodal approaches enable the study of clinical samples at a variety of molecular and spatial scales. The molecular complexity on the genome, proteome and metabolome level all needs to be taken into account. The distribution of several hundreds of molecules on the surface of complex (biological) surfaces can be determined directly in complementary imaging MS experiment with MALDI and SIMS. This enables molecular pathway analysis as well as the analysis of the role and evolution of the different molecular signals during e.g. tumor development.
Wednesday @ 4:00 PM in Sierra
Emerging Methods for Orthogonal Workflow Compatible Automated and Semi-Automated Cytological, Histological, and Analytical Sample Evaluation
Mariam Elnaggar - Prosolia (elnaggar@prosolia.com)

The continuous in situ microextraction provided by the flowprobe system facilitates atmospheric pressure sampling without additional extensive preparation for spot based targeted profiling as well as arrayed extractive analysis and scanned extractive profiling. Characterizations of surfaces by way of direct extraction, ionization, and identification of molecules of interest also is possible from histologic and cytological preparations in such a way that the samples are preserved and useful for subsequent orthogonal analysis. Presented here is an overview of various applications of the sample introduction technique at the levels of basic and quantitative research, biomarker discovery, drug deposition analysis, and clinical use.

Wednesday @ 4:20 PM in Sierra
Why the Operating Room Needs Mass Spectrometry (And Doesn’t Even Know It)
Alyssa Burgart - Stanford University (aburgart@stanford.edu)

There are gaps in information during surgical procedures in which the promise of mass spectrometric analysis can provide surgeons and anesthesiologists with perhaps their most powerful tool: actionable information. This talk is an invitation to MS practitioners to think outside the laboratory to explore the potential applications of MS in the operating room, from simple sedation cases to organ transplantation. Promising research on these techniques is already in development and this talk will serve to address potential future, wide use application.

Wednesday @ 4:40 PM in Sierra
Real-time Classification of Ex-vivo Breast Tissues by Rapid Evaporative Ionization Mass Spectrometry with a Combination of Electrosurgical Modalities
Edward St John - Imperial College (edward.stjohn@imperial.ac.uk) -- *Young Investigator Grantee*

Rapid Evaporative Ionization Mass Spectrometry (REIMS) measures the tissue specific ionic content of the electrosurgical smoke plume for the rapid identification of dissected tissues. Aerosol was aspirated from histologically validated ex-vivo breast samples for mass spectrometric analysis. Multivariate statistics were used for computational analysis of the data. A combination of “Cut” and “Coag” electrosurgical modalities corresponding to 280(cut)/281(coag) normal spectra, 80(cut)/59(coag) tumour spectra gave sensitivities of 92.5%(cut)/ 93.2%(coag) and specificity of 97.9%(cut)/95.7%(coag). A combined Cut & Coag model together with recognition software has enabled the real-time classification of ex-vivo breast tissues with a very high accuracy. The iKnife has been developed for real-time analysis of heterogeneous breast tissue in both cutting and coagulation electrosurgical modalities.
Effective Strategies for Overcoming Polyatomic Spectral Interferences During the Measurement of Trace Metals in Whole Blood Samples by ICP-MS

Brooke Katzman - Mayo Clinic (katzman.brooke@mayo.edu) -- *Young Investigator Grantee*

• The analysis of trace metals in blood samples by inductively coupled plasma-mass spectrometry (ICP-MS) can be complicated by number of unique challenges—both pre-analytical and analytical in nature. Not only should samples for analysis be collected in metal-free tubes to minimize contamination, but also special precautions must be taken to reduce the effect of polyatomic spectral interferences inherent to ICP-MS. Three approaches are commonly employed to overcome such interferences: 1) selection of isotopes that are free from interference, 2) incorporation of correction equations, and 3) the use of cell technology (i.e. collision cells or dynamic reaction cells). The above approaches were effectively utilized in the development of two robust assays to accurately and precisely quantitate chromium/cobalt and titanium in whole blood samples from patients with metal-on-metal implants.

Quantification of 15N-nitrite and 15N-nitrate in Human Biological Matrices: An LC-MS/MS Application to Study the Development of Nitrate Tolerance

Elizabeth Axton - Oregon State University (axtone@oregonstate.edu) -- *Young Investigator Grantee*

• Glycerol trinitrate (GTN) is a prodrug that is metabolized by xanthine oxidase (XO) to release nitric oxide (NO), inducing vasodilation in patients with cardiovascular diseases. Patients develop tolerance to GTN after a few weeks. We hypothesize that inactivation of XO by oxidative stress impairs GTN metabolism, which can be prevented with allopurinol (inhibitor of the molybdenum site of XO) and vitamin C (scavenger of reactive oxygen species). Our strategy is to quantify nitrite and nitrate, the stable metabolites of NO, as an endpoint of GTN metabolism. Our novel LC-MS/MS method quantifies 15N-nitrite and 15N-nitrate with a LLOQ of 1 nM. Isotope labeling removes interference from high background levels of nitrite and nitrate. We demonstrate that vitamin C and allopurinol can prevent nitrate tolerance in human endothelial cells, and the co-treatments enhance nitrite production from XO.

Taking the Hit Out of HIT: Heparin Induced Thrombocytopenia Assessment via LC-MS/MS Analysis of Endogenous Serotonin Release

Matthew Crawford - Labcorp (crawfm1@labcorp.com)

• Heparin-induced thrombocytopenia (HIT) is an antibody-mediated complication of heparin therapy caused by immunization against platelet factor 4 complexed with heparin. The serotonin release assay using washed-platelets is a functional assay and considered the gold standard, however, it’s highly complex and requires a radioactive doping of a donor platelet solution. We’ve developed and validated a method which incorporates the measurement of endogenous release of serotonin created by patient sera without the need for exogenous doping or radioactive labeling. 94% clinical concordance proves that by LC-MS/MS analysis of endogenous serotonin release could be an equivalent measure of HIT without the added complexity.
Part 1: Introduction to Clinical Proteomics  
Timothy Collier - Cleveland Heart Lab, Inc. (tcollier@clevelandheartlab.com)
- This session is directed toward attendees new to mass spectrometry and its use for measuring of proteins and peptides (proteomics) in the clinical laboratory. It will be presented in three parts with questions and discussion welcomed after each. Part one of this session will present the definition of proteomics within the broader context of systems biology. We will also discuss the clinical proteomics workflow within the context of the clinical laboratory environment, and how information gathered from proteomic measurements can offer clinical insight into a patient’s state of health, compared and contrasted to genetic, metabolic, and other small molecule diagnostics.

Part 2: Introduction to Clinical Proteomics  
Timothy Collier - Cleveland Heart Lab, Inc. (tcollier@clevelandheartlab.com)
- A mass spectrometer is more than a box with specimens going in and a numbers coming out. This part of the session will discuss a few of the most used types of mass spectrometers in the clinical laboratory and how they perform their measurements in the context of proteomic diagnostics. This includes: [1] Protein/Peptide ionization, [2] Guiding ions through the instrument, [3] Fragmentation (MS/MS), [4] Detection, and [5] Tools for Data Interpretation.

Part 3: Introduction to Clinical Proteomics  
Timothy Collier - Cleveland Heart Lab, Inc. (tcollier@clevelandheartlab.com)
- The final segment of this session will discuss the use of mass spectrometry-based proteomics for clinical applications with examples from the literature and real-world applications. Specific attention will be given to technological and performance advantages of those methods and how otherwise unmet clinical needs are addressed. This segment will conclude with an overview of new techniques, technologies, and development strategies that present opportunities for further advancement in the field.
Development of a Mass Spectrometry Method for Quantifying Glycoprotein in Ebola Virus-Like-Particles

Michael Ward - USAMRIID (protid@comcast.net)

- Virus-like particles (VLPs) are a promising vaccine platform composed of a subset of viral components that mimic the wild-type virus structure but lack genetic material. Ebola VLPs are produced by expressing recombinant Ebola viral glycoprotein (GP) and Ebola viral matrix protein VP40 in culture. Ebola VLPs protect non-human primates from lethality after Ebola challenge when administered as a vaccine. In order to better predict the success of each VLP lot, we developed a mass spectrometry method to quantify the amount of Ebola glycoprotein. Our results revealed a strong correlation between survival and the total amount of full length viral glycoprotein.

Detection and Discovery of Early Markers of Ebola Virus Infection Using Serum Proteomic Analysis

Lisa Cazares - USAMRIID (lisa.h.cazares.ctr@mail.mil)

- For the discovery of early markers of Ebola virus infection we have interrogated plasma from non-human primates (NHP) collected at multiple time-points during infection. Our experimental strategy employed 6-plex TMT labels for the quantitation of host proteins at pre-infection levels and 5 post-infection time-points. We discovered plasma proteins that change expression during Ebola infection in 7 NHP sample sets. Several acute phase proteins were induced systematically prior to the detection of serum viremia. Comparison of the Ebola NHP host response to that observed in Burkholderia pseudomallei infected NHP resulted in the discovery of unique differentially expressed proteins between these two infection types.

Bloodborne Pathogen Contamination in the Era of Laboratory Automation and Ebola

Andrew Bryan - University of Washington (andrewbb@uw.edu) -- *Young Investigator Grantee*

- The Centers for Disease Control (CDC) states that laboratory testing for persons under investigation for Ebola virus disease can be safely performed using automated laboratory instruments by adhering to bloodborne pathogen practices. We assessed contamination of a clinical chemistry total laboratory automation system by Hepatitis B and C viruses occurring through routine clinical use and after processing high-titer Hepatitis C-positive specimens. Contamination was detected primarily in association with a decapper instrument, but was also found in other locations including exposed surfaces. These data suggest a need for more detailed guidance regarding the handling of specimens potentially positive for Ebola virus.
Thursday @ 11:00 AM in Madera

**Gingerbread Men: A Cookie-cutter Bottom-up Proteomics Workflow for the Hungry?**

*Andy Hoofnagle - University of Washington (ahoof@u.washington.edu)*

- To test the hypothesis that a widely-used monoclonal immunoassay for vitamin D binding globulin (VDBG) was significantly affected by common polymorphisms, we developed a bottom-up proteomics assay. The method was validated according to our recently recommended guidelines for publication of novel biomarkers (Clinical Chemistry) and was used to quantify VDBG and determine the haplotype in samples accrued from a clinical research study that had been previously genotyped and analyzed by immunoassay. We have now applied the same workflow to other proteins and progress toward generating a plug-and-play workflow for medium- and high-abundance proteins in human serum/plasma will be discussed.

Thursday @ 11:20 AM in Madera

**Design of a LC-MS/MS Plasma Protein Assay Using Data Independent Acquisition**

*Jarrett Egertson - University of Washington (jegertso@uw.edu)*

- A data independent acquisition (DIA) approach is used to generate a highly multiplexed plasma protein assay. Using DIA, we build a chromatogram library containing relative fragment ion abundances and retention times for thousands of peptides detected in human plasma. Significantly, we use the high multiplexing capacity of DIA to expedite assay validation including assessment of digestion kinetics, peptide stability, and quantitative linearity. Additionally, we demonstrate an external calibration approach for DIA-based assays using a pooled plasma standard. The plasma standard is measured intermittently using a single LC-MS/MS DIA injection. The signal for each peptide measurement can then be calibrated to the signal for the same peptide in the plasma standard to control for batch effects and normalize to a common reference.

Thursday @ 11:40 AM in Madera

**An Empirical Approach to Signature Peptide Choice for Selected Reaction Monitoring: Quantification of Uromodulin in Urine**

*Jennifer Van Eyk - Cedars Sinai Medical Center (jennifer.vaneyk@cshs.org)*

- There are many proposed avenues for a seamless transition between biomarker discovery data and selected reaction monitoring (SRM) assays for biomarker validation. Unfortunately, studies with the abundant urinary protein uromodulin and albumin showed that these methods do not converge on a consistent set of surrogate peptides for targeted MS. As an alternative, we present an empirical peptide selection workflow for robust protein quantitation. Comparing the apparent abundance of a plurality of peptides derived from the same target protein makes it possible to select signature peptides that are unaffected by the unpredictable confounding factors that are inevitably present in biological samples. We are developing an algorism to select correlated and quantitative peptides for SRM/MRM analysis.
An Accurate Mass Imaging MS Approach to Support Preclinical PK/PD Assessments
Sheerin Shahidi-Latham - Genentech, Inc. (sheerink@gene.com)

This seminar will provide an overview of label-free high resolution mass spectrometric applications in support of drug discovery and development. Examples will include imaging MALDI MS of dosed tissues in support of effective drug delivery evaluations, highlighting the accurate mass approach for the simultaneous detection of drug and metabolites, and additionally the detection of endogenous components that provide a means for simultaneous PK/PD assessments while retaining spatial resolution. A synopsis of the advantages of high-resolution mass spectrometry, as well as, the technical challenges and opportunities in the context of the pharmaceutical industry will be discussed.

Mass Spectrometric Innovations for Tissue Imaging and Direct Analysis
Richard Yost - University of Florida (ryost@ufl.edu)

Mass spectrometric imaging (MSI) provides a level of chemical information unmatched by any other imaging modality (including histopathology, MRI, and PET scans). Furthermore, MSI offers the potential for rapid and direct analysis of tissue even when an image is not of interest. This presentation will explore innovations in MSI and direct tissue analysis, focusing on new sampling methods (including real-time in situ microextraction using the flowprobe and desorption electrospray or DESI) and strategies for increasing the speed, spatial resolution, information content, and quantitative performance of the methods. Applications to be discussed will include characterization and biomarker detection in melanoma, pansteatitis, aging muscle, and Parkinson’s disease.

Advancing Drug Development and Understanding Using Advanced Mass Spectrometry
Jeremy Norris - Vanderbilt University School of Medicine (j.norris@vanderbilt.edu)

Mass spectrometry technologies have advanced significantly, allowing for sensitive and specific measurements of drugs as well as their impact on biological systems. Current instrumentation and methodologies in imaging mass spectrometry now allow for the study of biology at the cellular level, the tissue level, and the level of a whole organism. These capabilities provide the opportunity for molecular understanding about complex drugs mechanisms and interactions that have not previously been available to drug developers. This presentation overviews these advances, provides example of their use, and discusses the prospects for transitioning these technologies to aid in drug development.
A Controlled Flow 96 Well Plate for Automation of Antibody Capture and Protein Digestion with Quantitative Determination of Surrogate Peptides by LCMSMS

John Laycock - SPEware Corporation (john.laycock@speware.com)

We present a novel automated workflow utilizing 96 well plates with control flow properties for immunoaffinity capture and tryptic digestion. The novel plate airgap design restricts the flow of liquid during conditions applicable to many assay incubation types and steps. The flow is restricted completely until positive pressure is applied, providing a simple and cost-effective alternative to magnetic bead based cleanup protocols. In this presentation we discuss application of controlled-flow plates (CFP) to immunoaffinity capture of a recombinant human antibody for isolation from rat plasma, followed by tryptic digestion and LCMSMS.

Accelerating Mass Spectral Analysis: The Sample Preparation Component

Fred Regnier - Purdue University (fregnier@purdue.edu)

A new form of antigen separation, mobile affinity sorbent chromatography (MASC) will be described that accelerates immune complex purification for analysis by MALDI-MS. This is achieved in 15 sec using 1-20 antibodies covalently linked to a soluble sorbent that subsequent to antigen binding produces a supramolecular complex in the range of 1000 kD. When introduced into a size exclusion column complexes are excluded from pore matrices, being washed continuously with fresh solvent during migration while lower affinity species dissociate and are resolved. Complexes thus resolved are continuously mixed with MALDI matrix and deposited on the MALDI plate.

Getting the Biggest Bang for the Buck: Manipulating Trypsin Digestion Conditions to Accelerate Digestion and Improve Signal Intensity

Yu Zi (Emma) Zheng - St.Paul's Hospital, University of British Columbia (zhengemma@gmail.com) -- *Young Investigator Grantee*

Protein digestion is a critical step in sample preparation prior to mass spectrometric analysis of proteins. Trypsin is the most commonly used protease in proteomics experiments; however digestion can be highly variable and is dependent on several factors including digestion buffer, denaturants, trypsin type, and sample type. Historically, trypsin digestion protocols have relied on lengthy digestion times, which are inappropriate for many clinical applications. We evaluated numerous iterations of digestion conditions for five plasma proteins and examined which changes yielded the greatest improvement in signal, reproducibility of the digestion profile, and rapid release of proteolytic peptides. It is our hope that this data can help clinical laboratorians accelerate the development phase of novel targeted assays by identifying practical approaches to improving digestion protocols.
Development and Validation of an LC-MS/MS Sulfonylurea Assay for Hypoglycemia Cases in the Emergency Department

He Yang - UCSF General Hospital (heyang2008@u.northwestern.edu) -- *Young Investigator Grantee*

Detection of the presence of sulfonylurea-type oral antidiabetics allows for the differential diagnosis of hypoglycemia of unknown origin and rules out other pathophysiology conditions. We developed and validated a qualitative LC-MS/MS assay to detect sulfonylureas in serum. Compounds were identified by retention time, two MRM transitions and an ion ratio. Linearity, LOD, precision, matrix effect, recovery, carry-over and stability of the final method were evaluated. Method comparison studies with an outside reference laboratory using 51 authentic patient samples revealed a correlation coefficient of 0.99. The assay had been utilized in 19 hypoglycemia cases in the ED and assisted differential diagnosis.

Real-time PK Measurement of the Chemotherapeutic Drug Melphalan in Whole Blood by a Novel PaperSpray-tandem Mass Spectrometry (PS-MS/MS)

Junfang Zhao - Cincinnati Children's Hospital Medical Center (junfang.zhao@cchmc.org) -- *Young Investigator Grantee*

PaperSpray (PS) is an ionization technique that generates gas phase ions directly from a dried blood spot or other fluids without the need for sample pretreatment and chromatography. We describe a simple and rapid PS-MS/MS method for real-time measurement of the chemotherapeutic drug melphalan in blood from patients undergoing hematopoietic stem-cell transplantation. Our aim was to determine the optimum target range for melphalan in the pediatric population. PS-MS/MS had excellent linearity of response over large dynamic range, high precision and accuracy. In a pharmacokinetic study of melphalan PS-MS/MS correlated well with ESI-LC-MS/MS but had the advantage of speed of analysis.

Development and Validation of Anti-TB Drugs in Plasma to Support Pharmacokinetic-Driven Studies

Mark Marzinke - Johns Hopkins University School of Medicine (mmarzin1@jhmi.edu) -- *Young Investigator Grantee*

In order to better understand the pharmacokinetic-pharmacodynamic (PK-PD) relationships of anti-tuberculosis drugs in disease management, PK studies are required to assess drug concentrations. Thus, liquid chromatographic-tandem mass spectrometric (LC-MS/MS) methods for the multiplexed quantification of the common anti-TB medications rifampin (RIF), pyrazinamide (PZA), ethambutol (EMB), as well as the fourth-generation antibacterial agent moxifloxacin (MOX) and the experimental drug PA-824 in plasma have been developed and validation according to the recommendations of the FDA, Guidance for Industry: Bioanalytical Method Validation document. Further, the described work illustrates the bioanalytical considerations in working with these compounds.
Thursday @ 1:00 PM in Mojave Learning Center

**Part 1: MALDI-TOF Mass Spectrometry in the Clinical Microbiology Laboratory**

*Lori Bourassa - University of Washington Medical Center* (bourassa@uw.edu) -- *Young Investigator Grantee*

Matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS) is a rapid, accurate and high throughput method for microorganism identification. MALDI-TOF MS identification of microorganisms has revolutionized the clinical microbiology laboratory offering species-level identifications in minutes with accuracy that matches and often exceeds that of conventional identification systems. In this session, we will present case studies that demonstrate both the clinical utility and the diagnostic pitfalls of MALDI-TOF MS in the clinical microbiology laboratory and discuss "interesting" results acquired as a result of widespread use of this identification method.

Thursday @ 1:20 PM in Mojave Learning Center

**Part 2: MALDI-TOF Mass Spectrometry in the Clinical Microbiology Laboratory**

*Melanie Yarbrough - Washington University in St. Louis* (myarbrough@path.wustl.edu) -- *Young Investigator Grantee*

Matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS) is a rapid, accurate and high throughput method for microorganism identification. MALDI-TOF MS identification of microorganisms has revolutionized the clinical microbiology laboratory offering species-level identifications in minutes with accuracy that matches and often exceeds that of conventional identification systems. In this session, we will present case studies that demonstrate both the clinical utility and the diagnostic pitfalls of MALDI-TOF MS in the clinical microbiology laboratory and discuss "interesting" results acquired as a result of widespread use of this identification method.
Thursday @ 1:00 PM in Catalina
**Successes and Challenges of Metabolic Reprogramming Elucidation in Cancers Directly from Human Subjects via Stable Isotope Resolved Metabolomics (SIRM)**

*Richard Higashi - University of Kentucky (rick.higashi@uky.edu)*

Elucidating metabolic reprogramming in cancers requires functional omics, especially metabolomics. Most metabolites have numerous roles, such that their chemical identity alone cannot establish their biochemical identity. Stable isotope resolved metabolomics (SIRM) can distinguish among pathways and functions. Using SIRM we have mapped glucose C utilization in resected tumor and non-tumor tissues from lung cancer patients infused with [U-13C]-glucose, plus C,N utilization in their tissue slices with [U-13C]-glucose or [U-13C,15N]-glutamine. This revealed many details, including up regulation of pyruvate carboxylase anaplerosis. The paired human tissue slice platform is being used with drug candidates to test impacts on metabolic reprogramming.

Thursday @ 1:20 PM in Catalina
**Combining Microfluidic Separations with High Pressure Mass Spectrometry for Clinical Diagnostic Applications**

*J. Scott Mellors - 908 Devices, Inc. and University of North Carolina (mellors@908devices.com)*

We are attempting to move LC-MS analyses out of the core lab by combining microfluidic capillary electrophoresis with high pressure mass spectrometry. Combining these two miniaturized technologies yields a system that can fit on the benchtop of nearly any lab and can be operated by a non-expert. The integration of sample injection, separation and electrospray ionization in a single glass microchip enables extremely fast and efficient separations; while operation of miniaturized ion traps at high pressure (~1 Torr) removes the need for large and expensive pumping systems. We are developing fully automated assays on this platform for a range of applications. Of particular relevance are newborn screening for inborn errors of metabolism; and monitoring pain management. Recent results will be presented for both of these applications.
Scaling Discovery Proteomics to Large Lung Cancer Cohorts Using Data Independent Acquisition

John Koomen - Moffitt Cancer Center (john.koomen@moffitt.org)

* Discovery proteomics using data independent acquisition (DIA) provides the maximum content from a single LC-MS/MS analysis. After a pilot project to compare DIA to discovery proteomics using traditional data dependent acquisition techniques, DIA strategies have been optimized and applied to 2 cohorts of lung cancer patients. The biology of the proteome detected and quantified in DIA experiments has been explored, and the resulting data have been used to classify lung cancer patients by their proteomic phenotypes. Feasibility has also been demonstrated for analysis of tissue microarrays using this technique, producing quantitative data for >3,000 proteins from a single section of a lung tumor core (0.6 mm in diameter and 5 microns thick). These data indicate the potential utility of DIA for assessment of tumor biology in situ using archived tumor specimens.

Analytical Characterization of Multiplexed Parallel Reaction Monitoring Assays to Quantify N-linked Glycosite-containing Peptides in Serum

Stefani Thomas - Johns Hopkins University (stoma92@jhmi.edu) -- *Young Investigator Grantee*

* Protein glycosylation is one of the most common protein modifications, and the quantitative analysis of glycoproteins has the potential to reveal biological functions and their association with disease. However, the high throughput accurate quantification of glycoproteins is technically challenging due to the scarcity of robust assays for their detection and quantification. We developed and characterized 43 multiplexed parallel reaction monitoring (PRM) assays that were used to quantify formerly N-linked glycosite-containing peptides from 37 proteins in serum from prostate cancer patients. The assays were characterized by performance metrics and criteria established by the NCI’s Clinical Proteomic Tumor Analysis Consortium (CPTAC) to facilitate the widespread adoption of the assays in studies designed to confidently detect changes in the relative abundance of these analytes.
Desorption Electrospray Ionization – Mass Spectrometry for Intraoperative Analysis of Brain Cancer Tissue

Alan Jarmusch - Purdue University (ajarmusc@purdue.edu) -- *Young Investigator Grantee*

- Surgical intervention is a primary treatment option for brain tumors. The best patient outcomes are dependent on absolute tumor resection, ideally minimizing damage to adjacent normal tissue, and reducing surgery time. Ambient ionization MS provides molecular-based diagnostics on a timescale compatible with surgery. We have developed new DESI-MS methodology for the analysis of smeared neural tissue biopsies during tumor resection. MS data acquisition for each sample required <2 minutes, while providing rich lipid and metabolite MS profiles. Multivariate statistics and a DESI-MS spectral library, compiled with disease states as validated by traditional histopathology, was used in predicting disease state.

Multimodal Imaging Mass Spectrometry for Probing Aβ-Plaque Pathology in Transgenic Alzheimer’s Disease Mice

Jörg Hanrieder - University of Gothenburg (jh@gu.se) -- *Young Investigator Grantee*

- The pathological mechanisms underlying Alzheimer’s disease are still not understood. The disease is characterized by accumulation and aggregation of amyloid peptides into extracellular plaques. The factors that promote neurotoxic amyloid peptide aggregation remain elusive. In the present study, multimodal (SIMS and) MALDI imaging was used to study individual amyloid plaques in brain tissue from in brain sections of transgenic AD mice (tgARCSWE) in order to elucidate the plaque associated chemical microenvironment. PCA image analysis was used to interrogate the IMS data set for identifying anatomical features based on their chemical identity. Statistics on spectral data of regions of interest reveal brain region specific changes in amyloid peptide pathology and lipid content. This was further verified using immunohistochemistry and laser micro dissection and MALDI MS of plaque extracts.
Don’t Manually Transcribe Your Results: The Poor Person’s Guide to LC-MS/MS LIS Interfacing with R  
Daniel Holmes - University of British Columbia (dtholmes@mail.ubc.ca)

At present, LC-MS/MS vendors do not have upload/download capabilities to laboratory information systems (LIS). As a result, though tremendous energy is often spent in development of accurate, precise and robust LC-MS/MS methods, the results themselves are manually transcribed. This work is both demoralizing and error-prone. A simple approach to instrument datafile processing is presented using the R statistical programming language. Identification of patient results, calibrator, and QC is shown. Handling of non-numeric results is discussed. Potential hazards will be reviewed. Suppression of ion-ratio failures and the appending of interpretive comments are demonstrated. Source code will be available for free use or modification.

Clinical Quality Control for Multiplex Mass Spectrometry  
Stephen Master - Weill Cornell Medicine (srn9012@med.cornell.edu)

The development of novel, highly multiplex assays has led to the possibility of new clinical assays with improved sensitivity / specificity, decreased sample size requirements, and reduced assay cost per analyte. While these clinical assays have potential diagnostic advantages, they have raised a new set of problems for traditional laboratory quality control (QC) paradigms. We will present four multiplex QC paradigms that address these challenges. Further, we will discuss the fundamental distinction between patterns (multiplex tests with associated bioinformatics classifiers that yield one of a small number of diagnostic outcomes) and panels (multiplex tests that are the equivalent of a series of uniplex tests).
Thursday @ 1:00 PM in SmokeTree

**Using Mass Spectrometry to Understand Cystic Fibrosis as a Protein Misfolding Disease**

*John Yates* - *The Scripps Research Institute (jyates@scripps.edu)*

- Recent studies on the loss of function mutant form of the Cystic Fibrosis Transport Regulator (ΔF508) as it progresses through the folding pathway will be presented. Through the study of protein-protein interactions and modifications that regulate maturation of CFTR, we are beginning to understand the critical interactions regulating pathways for export or destruction.

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Thursday @ 1:20 PM in SmokeTree

**Dried Blood Spot Screening for Wilson Disease Using Immuno-SRM**

*Sunhee Jung* - *Seattle Children (sunhee@uw.edu)*

- Wilson Disease (WD), a copper transport disorder caused by a genetic defect in the ATP7B gene, has been a long time candidate for newborn screening because of proven interventions that give better results when carried out early in life, preventing life-long neurological disability and/or liver cirrhosis. WD presents with absent or significantly diminished ATP7B protein that is localized in the transmembrane. ATP7B has enormous potential for screening of WD if the protein can be identified from dried blood spot (DBS) samples. We herein report a proof-concept study demonstrating that the immuno-SRM platform can detect ATP7B in DBS and the assay readily distinguishes affected cases from normal controls. Our promising data opens up the great potential of a multiplexed immuno-SRM assay for screening a variety of congenital disorders lacking specific protein markers in DBS.
Thursday @ 2:00 PM in Catalina
An Unbiased Investigation of the Lipidomic and Metabolomic Pathways Altered in Alzheimer’s Disease Brain
Giuseppe Astarita - Georgetown University (giuseppe_astarita@waters.com)

Alzheimer's disease (AD) is the most common cause of adult dementia, but the complete set of molecular changes accompanying this inexorable neurodegenerative disease remains still elusive. Here we used an unbiased lipidomics and metabolomics approach to survey frozen frontal cortex samples from clinically characterized AD patients (n=21) and age-matched controls (n=19). Our study highlights specific biochemical pathways that are altered in the brains from individuals with AD compared to control subjects, supporting future venues of investigations.

Thursday @ 2:20 PM in Catalina
Potential of Metabolome Analysis for Early Diagnosis of Alzheimer’s Disease
Therese Koal - Biocrates Life Sciences AG (therese.koal@biocrates.com)

There is a strong need for pre-symptomatic biomarkers in Alzheimer’s disease (~20 years before manifestation) due to the very progressive disease character and the lack of therapy at current time point of diagnosis. Targeted metabolomics has the potential to improve the current diagnosis in cerebrospinal fluid (CSF) and use metabolic signatures as (early) disease detection in blood for population screening approach. Therefore, appropriate studies in CSF and blood were performed. In the result, SM could be indentified as potential markers in CSF and PC and lyso PC as metabolic signature in blood. Alteration of PC and lyso PC are linked to phospholipase A2 (PLA2) because PLA2 catalyze cleavage of fatty acids from sn-2 position of phospholipids producing free fatty acids and lyso PC. Data will be presented and hypothesis of PC and lyso PC related to PLA2 will be discussed.
Analysis of ‘Total’ Vitamin D Binding Protein and Albumin with Simultaneous Identification of VDBP Isoforms Using Rapid Trypsin Digestion and TurboFlow LC-MS

**Lewis Couchman** - King’s College Hospital (lewis.couchman@nhs.net) -- *Young Investigator Grantee*

* Analysis of vitamin D binding protein (VDBP) may be a useful adjunct to measuring total serum 25-hydroxyvitamin D concentrations in assessing vitamin D status. We have developed a method for the measurement of ‘total’ VDBP using ‘non-specific’ tryptic peptides with qualitative identification of isoforms using isoform-specific tryptic peptides. Whole serum samples were digested using SMART Digest™ kits at 70°C (30 min), and digests diluted with isotope-labelled peptides prior to direct analysis by TurboFlow LC-MS. This method also allows for simultaneous quantitation of ‘total’ serum albumin, which may be an additional factor useful in calculating a ‘free vitamin D’ index.

Differential MS and Targeted MS/MS Used to Identify an Aberrant ACTH Isoform

**Mari DeMarco** - Univ. of British Columbia, St Paul’s Hospital (mdmarco@mail.ubc.ca) -- *Young Investigator Grantee*

* To identify a suspected circulating non-functional ACTH isoform in an individual with a silent corticotroph adenoma, we developed a differential mass spectrometry (dMS) and targeted MS/MS approach. For dMS experiments, we compared ACTH immunoprecipitated from the individual in question, to the plasma from individuals with elevated ACTH and typical manifestations of ACTH excess. MS experiments revealed the presence of a truncated form of ACTH and MS/MS was used to confirm the identity of both the wild-type and aberrantly processed ACTH isoform. This dMS—MS/MS approach has the potential to be applied broadly in cases of structurally abnormal ACTH production.
Thursday @ 2:00 PM in Pasadena

**Translating DESI-MSI to Clinical Pathology – Adventures and Challenges**

*Zoltan Takats - Imperial College London (z.takats@imperial.ac.uk)*

» Feasibility of embedding DESI-MSI into clinical histopathology environment was tested. Interlaboratory studies revealed that the information content of results is largely independent from the analysis site, making the world-wide standardization of the method possible. Experiments aimed at the use of FFPE samples were also successfully performed, leading to improved compatibility with current histological practice. Furthermore, the speed and the resolution of the method were also improved to turn DESI-MSI into a histology friendly approach.

Thursday @ 2:20 PM in Pasadena

**Mass Spectrometry for Image Guided Neurosurgery and Drug Development**

*Nathalie Agar - Brigham and Women's Hospital, Harvard Medical School (Nathalie_Agar@dfci.harvard.edu)*

» Mass spectrometry provides multiple options for the direct characterization of tissue to support surgical decision-making, and provides significant insight in the development of drugs targeting tumors of the central nervous system (CNS). Using an array of mass spectrometry (MS) applications, we rapidly analyze specific tumor markers such as metabolites, fatty acids, lipids, and proteins from surgical tissue for surgical guidance and rapid diagnosis. Using similar clinical protocols, we visualize drug and metabolites penetration in brain tumor tissue and correlate with tumor heterogeneity and response to support drug development.
The Future of Mass Spectrometry-based Protein Lab Tests

Dobrin Nedelkov - Arizona State University (dobrin.nedelkov@asu.edu)

• Mass spectrometry (MS)–based approaches have produced an increasing number of protein biomarker candidates. Yet, vast majority of these biomarkers have not been validated and translated into routine lab tests. To date, there are less than a dozen MS-based protein clinical lab tests. Discussed here will be the key aspects for development, validation and translation of MS-based lab tests into the clinical laboratory: the demand, end-users, platforms, sample preparation, design, validation, and regulatory issues. An emphasis on content, simplicity, and cost seems to be critical for clinical adoption of MS-based protein lab tests. Some possible killer-apps and solutions will be discussed.

MALDI TOF Mass Spectrometry as a Tool for In Vitro Testing

Mark Duncan - School of Medicine, University of Colorado (mark.duncan@ucdenver.edu)

• MALDI-TOF MS, an established technique for analyzing nonvolatile molecules, has limited acceptance for clinical applications as a qualitative tool due to the widespread belief that MALDI-TOF is not quantitative. However, modern MALDI-TOF mass spectrometers generate reproducible data that can be used for accurate quantification of components in complex samples, such as whole blood and urine. Clinical MALDI applications require a very small volume of sample (e.g., 1 µL), and in some instances workup can be as simple as dilution. Other applications may require addition of an internal standard or purification and concentration of the analyte(s). Clinical assays illustrating each of these cases will be described.
Keynote Presentations

• Session 8 • Track 2 •
The Microbiome Metabolome Interface
Thursday @ 3:00 PM in Catalina
Session Chair: Karen Phinney - NIST

Thursday @ 3:00 PM in Catalina
3D Cartography of the Microbiome of the Human Skin and Lungs in Cystic Fibrosis
Pieter Dorrestein - UCSD (pdorrestein@ucsd.edu)

- The microbiome is critical to human health yet we know little about the chemical environment that our microbes live in. In this presentation we will explore untargeted metabolomics strategies to reveal the chemical environment of the microbiome. First we will cover the 3D skin metabolome and how the skin metabolome is influenced by personal care, medications, diet and the microbiome. We will explore the chemical similarities and contrasts associated with the chemistry from the skin of people who do not use medications or personal care products. Secondly we will highlight the metabolome of a human lung associated with Cystic Fibrosis in 3D. Finally the presentation will present a case study of a CF patient that clinically cultured Pseudomonas but that ultimately passed due to an E.coli infection.

• Session 8 • Track 3 •
Innovative Topdown Protein Analysis
Thursday @ 3:00 PM in Madera
Session Chair: John Yates - Scripps Research Institute

Thursday @ 3:00 PM in Madera
Innovative Instrumentation and Methods for the Identification of Intact Proteins in Mixtures and for Sequence Analysis of Antibodies and Posttranslationally-Modified, Intact Proteins on a Chromatographic Time-Scale
Donald Hunt - University of Virginia (dfh@virginia.edu)

- This lecture will focus on data generated with a new ion source that facilitates simultaneous generation of positively charged sample ions by electrospray ionization and negatively charged reagent ions for both electron transfer dissociation (ETD) and ion-ion proton transfer (IIPT) reactions on Orbitrap mass spectrometers. Implementation of multiple C-trap fills for enhanced sensitivity will be discussed and both parallel peak parking, and ion ejection strategies to facilitate protein separation and enhanced sequence coverage of intact proteins will be described. Use of IIPT/ETD facilitates near complete sequence coverage on many intact proteins and is ideally suited for locating multiple posttranslational modifications on the same protein molecule. Sequence analysis of antibodies with an enzyme reactor that generates 3-10 KDa fragments in seconds will also be discussed.
We have employed IMS in studies of a variety of biologically and medically relevant research projects. One area of interest is the molecular mapping of molecular changes occurring in diabetes in both a mouse model and in the human disease. Major molecular alterations have been recorded in advanced diabetic nephropathy involving both proteins and lipids. Other applications include developmental studies of embryo implantation in mouse, assessment of margins in renal cancers as well as that in other organs, and neurodegenerative disease. Molecular signatures have been identified that are differentially expressed in diseased tissue compared to normal tissue and also in differentiating different stages of disease. These signatures typically consist of 10-20 or more different proteins and peptides, each identified using classical proteomics methods.

Sorbent-attached membrane funnel spray ionization method was a novel mass spectrometry technique for high sensitive, low cost, high throughput analysis of complex samples using in-situ solid-phase extraction cleanup process prior to membrane funnel spray ionization. The sample platform was made from low-cost disposable materials, such as Parafilm, and could easily accommodate tens to hundreds of samples. The sample deposition, cleanup and spray analysis could be automated. The method could also be used to generate chemical images from imprints developed on the sorbent-attached membrane. With multiple washings using solvents with increasing solvent strength, imaging of low-abundant or low polarity chemicals could also be obtained.
Posters by Topic

Please Find *Extended Poster Abstracts* under Posters by Day/Time (starting on page 96)

### Endocrinology

Endocrinology | Monday 7:00 PM Poster #2
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**Accuracy Evaluation of Routine Vitamin D Immunoassays Compared with LC-MS/MS in Pregnant Women and Intensive Care Unit Patients**
*Yeo-Min Yun* - Konkuk University School of Medicine

Endocrinology | Monday 7:00 PM Poster #6
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**Development and Validation of LC-MS/MS Method for Determination of Testosterone in Serum**
*Eun Hee Lee* - Green Cross Laboratories

Endocrinology | Monday 7:00 PM Poster #17
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**High Serum Lipids Cause Erroneously Low Total 25-OH Vitamin D Levels by a Chemiluminescent Immunoassay.**
*Joshua Hayden* - Weill Cornell Medical College

Endocrinology | Monday 7:00 PM Poster #21
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**Evaluation of Measurement for Serum 3-epi-25-hydroxyvitamin D3, 25-hydroxyvitamin D3 and 25-hydroxyvitamin D2 Using UPLC-MS/MS in a Korean Reference Laboratory**
*Sung Eun Cho* - LabGenomics Clinical Laboratories

Endocrinology | Monday 7:00 PM Poster #47
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**Method Validation for Quantitation of Testosterone Calibrators: A Modification of Reference Measurement Procedures**
*Ravi Orugunti* - Cerilliant

Endocrinology | Monday 7:00 PM Poster #83
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**Metanephrines in Urine by Liquid Chromatography Tandem Mass Spectrometry**
*Magdalena Rajska* - Spadia Lab

Endocrinology | Monday 7:00 PM Poster #87
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**Extraction of Urinary Hormone Metabolites from Urine Using Supported Liquid Extraction Prior to HPLC-MS/MS Analysis**
*Kristin Jones* - Biotage

Endocrinology | Tuesday 3:00 PM Poster #46
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**Interferences of Blood Collection Tubes in the Measurement of Androgen Concentrations After Administration of a Novel Androgen Ester**
*Jonas Ceponis* - Los Angeles Biomedical Institute at Harbor-UCLA

Endocrinology | Tuesday 3:00 PM Poster #62
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**Profiling Thyroid Hormones by LC/MS/MS Analysis in Various Preclinical Species and Humans**
*Lina Luo* - Pfizer, Inc.

Endocrinology | Tuesday 5:00 PM Poster #65
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**Quantitation of Serum 17-hydroxyprogesterone, Testosterone, Dehydroepiandrosterone and Androstenedione Using UPLC-MS/MS**
*Theresa Swift* - University of Michigan Health System

Endocrinology | Tuesday 5:00 PM Poster #71
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**High-sensitivity, High-Throughput Quantitation of Catecholamines and Metabolites in Plasma by Automated WCX-SPE Coupled to LC/MS/MS for Clinical Research**
*Ichiro Hirano* - Shimadzu Corporation
High-sensitivity, High-Throughput Quantitation of Catecholamines and Metabolites in Urine by LC/MS/MS for Clinical Research

Atsuhiko Toyama - MS Business Unit, Shimadzu Corporation

Determination of Etonogestrel in Blood Plasma by High Performance Liquid Chromatography - Mass Spectrometry

Irina Zolkina - Pirogov Russian National Research Medical University

Sex Steroid Hormone Stability: Gel versus Non-gel Tubes

Sophie Hepburn - Prince of Wales Hospital

Analysis of Urinary Free Catecholamines and Metanephrines by Tandem Mass Spectrometry: Validation and Implementation in a Clinical Laboratory

Anna Robson - Heart of England NHS Foundation Trust

Sensitive Measurement of Plasma 1,25-Dihydroxyvitamin D2&3 (125DHVD) via LC-MS/MS: A Simple SPE Sample Preparation and MS Sensitizing Derivatization Process

Qi Huang - Quantalytical Labs

Tackling the Interference Problem for Estradiol Analysis by LC-MS/MS, Using Differential Ion Mobility Spectrometry

Michael J. Y. Jarvis - Sciex

Generic Sample Preparation Methodology for the Analysis of Steroid Hormones by LC-MS/MS for Clinical Research

Dominic Foley - Waters Corporation

Development and Validation of a LC-ESI-MS/MS Quantification Method of 25-hydroxyvitamin D2&D3 and of their C3-epimer

Pierre-Luc Mallet - University of Montreal, CIUSSS-CHUS

A Total and Free Testosterone Method that Utilizes Automation and a Novel Microdialysis Plate to Achieve Efficient Workflow in a Clinical Laboratory

Jennifer Fahse - Mayo Clinic

Fat Soluble Vitamin Detection in Human Serum and Plasma by LC-MS/MS Using Biotage ISOLUTE SLE+ 96-well Plate Extraction

Jianqing (Ben) Lu - Prince of Wales Hospital

Steroid Hormones in Serum, a Simply, Accurate, Sensitive and Not Extractable Kit Ready to Use by LC-MS/MS

Stefano Sartori - Eureka srl - Lab Division
ICP-MS

ICP-MS | Monday 7:00 PM Poster #91
Challenges of ICP-MS Method Development for Routine Clinical Analysis
Joshua Akin - UC San Diego Health System

ICP-MS | Wednesday 5:00 PM Poster #41
Accurate and Precise Sample Introduction at the Micro-Level: A New Approach to Routine, High Throughput Analysis for Trace Element Quantification with ICP-MS
Peter Winship - Teledyne CETAC Technologies

Inborn Errors of Metabolism

Inborn Errors of Metabolism | Monday 7:00 PM Poster #62
Newborn Screening Tests for Metabolic Disorders Using Tandem Mass Spectrometry in Korea-Report from One Laboratory
Yoonjoo Kim - EONE Laboratories

Inborn Errors of Metabolism | Monday 7:00 PM Poster #81
Quantification of Gycosaminoglycans (CS, DS and HS) in Dried Urine Spots by UPLC-MS/MS
David Millington - Duke University Hospital

Inborn Errors of Metabolism | Tuesday 5:00 PM Poster #7
Liquid Chromatography Mass Spectrometry Applications in a Newborn Screening for Mucopolysaccharidoses
Francyne Kabaski - University of Delaware/ Nemours

Inborn Errors of Metabolism | Tuesday 5:00 PM Poster #49
An Improved Tandem Mass Spectrometry Method for GALC Enzyme Assay and Psychosine Analysis in Dried Blood Spots for Identification of Krabbe Disease
Hsuan-Chieh Liao - University of Washington

Inborn Errors of Metabolism | Tuesday 5:00 PM Poster #89
Preliminary Results from the Slovenian Expanded Newborn Screening Pilot Study
Andraz Smon - Biochemistry graduate

Inborn Errors of Metabolism | Wednesday 3:00 PM Poster #44
Detection and Direct Quantitation of Guanidinoacetate, Creatine and Creatinine in Human Urine by LC-MS/MS and Electrospray Ionization
Thomas Lynn - Quest Diagnostics, Inc. - Nichols Institute

Inborn Errors of Metabolism | Wednesday 3:00 PM Poster #48
The Role of Specimen Handling Time on the Interpretation of Plasma Acylcarnitine Profiles for the Diagnosis of Inborn Errors of Fatty Acid Metabolism
Tiffany Thomas - Columbia University Medical Center

Inborn Errors of Metabolism | Wednesday 3:00 PM Poster #60
Jia Wang - Thermo Fisher Scientific

Inborn Errors of Metabolism | Wednesday 3:00 PM Poster #72
Developed Method for Acylcarnitine Analysis in Serum Using LC-MS/MS as a Clinical Exam
Hironori Kobayashi - Shimane University Faculty of Medicine

Metabolomics

Metabolomics | Monday 7:00 PM Poster #3
Quantification of Testosterone in Serum by Liquid Chromatography-tandem Mass Spectrometry
Vasanta Putluri - Baylor College of Medicine
Identification of the Role of FraB in F-Asn’s Metabolism in Salmonella and Development of the Method to Extract and Quantify F-Asn from Mouse Feces  
**Jikang Wu** - Ohio State University

Separating Vitamin D2 D3, their 25-OH Metabolites and C-3 Epimers  
**Ken Tseng** - Nacalai USA Inc.

Metabolomic Profile Change in Type 2 Diabetes Revealed by Commercial Metabolomics Kit with Mass Spectrometry  
**Sang-Guk Lee** - Yonsei University College of Medicine

Discovering Diabetic Lipid Biomarker Using HRAM LC-MS-MS Approach on a High Field Hybrid Quadrupole-Orbitrap Mass Spectrometer  
**Reiko Kiyonami** - Thermo Fisher Scientific

A Novel Liquid Chromatography Mass Spectrometry Method for the Analysis of Succinate: Fumarate Ratios in the Detection of SDHx-associated Tumours  
**Talia Novos** - Prince of Wales Hospital, SEALS

The Application of Ion Mobility Mass Spectrometry to Lipidomics – a Demonstration of Instrumental Capabilities for a Diabetic Mouse Model  
**Julia Denes** - University of Cambridge

Uromics: Metabolomics in Urine for Seroquel®, Latuda®, and Haldol®  
**Erin Strickland** - Ameritox, Ltd.

A Workflow for Drug Discovery from Environmental Samples Using Molecular Networks  
**Stefano Bonissone** - Digital Proteomics LLC

Use of a Novel C18-Based Stationary Phase for Human Urine Metabolite Profiling by UHPLC-High Resolution Accurate Mass Spectrometry (HRAM)  
**Alan McKeown** - Advanced Chromatography Technologies Ltd

Change in Redox Balance Couples with Redistribution of Metabolic Flux to Protect Glutathione-deficient Gclm-knockout Mice from Alcoholic Liver Disease  
**Soumen Kanti Manna** - Saha Institute of Nuclear Physics

Discrimination of Diabetic Lipid and Metabolite Profiles in Plasma in the Zucker Rat Model Using PaperSpray-High Resolution Mass Spectrometry  
**Justin Wiseman** - Prosolia

Ion Mobility Mass Spectrometry: Alternative Drift Gas Selection for Improved Separation of Isomers in Clinical Analysis  
**Christopher Chouinard** - University of Florida
Metabolomics | Wednesday 5:00 PM Poster #61
Analyte or Amalgamation? Exploring Relationships and Redundancy in Metabolomic Datasets
Nathaniel Mahieu - Washington University

Microbiology/Virology

Microbiology/Virology | Monday 7:00 PM Poster #73
Identification of Anaerobic Bacteria from BACTEC and BacT/Alert Anaerobic Blood Culture Media Using the Bruker MALDI Sepsityper Kit and MALDI-TOF MS
Jogarao Vedula - Div. of Clinical Microbiology, Icahn School of Medicine

Microbiology/Virology | Monday 7:00 PM Poster #84
Categorizing and Differentiating of Clinically Isolated Mycobacteria by Differential Pattern Analysis of MALDI-TOF MS Data
Kyu Park - ASTA, Inc.

Microbiology/Virology | Tuesday 5:00 PM Poster #37
Identification of Nontuberculous Mycobacteria Species by Tinkerbell LT
Jae-Seok Kim - Hallym University

Microbiology/Virology | Tuesday 5:00 PM Poster #83
Measurement of Kynurenine-to-tryptophan Ratio as a Biomarker for Urinary Tract Infection
Melanie Yarbrough - Washington University School of Medicine

Microbiology/Virology | Wednesday 3:00 PM Poster #38
Rapid Evaporative Ionisation Mass Spectrometry (REIMS) as a Novel Approach to Microbial Community Profiling
Adam Burke - Imperial College, London

New Advances

New Advances | Tuesday 3:00 PM Poster #12
Quantification via Signature Peptides: The Advantage of Using Differential Ion Mobility Spectrometry
Evgeni Fedorov - Biotrial Bioanalytical Services

New Advances | Tuesday 5:00 PM Poster #17
Run Zhang Shi - Stanford University School of Medicine

New Advances | Tuesday 3:00 PM Poster #18
Reduction in Pipette Tip Consumable Cost and Waste Through Innovation
Ali Safavi - Grenova

New Advances | Tuesday 3:00 PM Poster #20
Comparison of Dried Blood Spot Collection Devices by Paper Spray Ionization Mass Spectrometry
Karen Cesafsky - Purdue University

New Advances | Tuesday 3:00 PM Poster #54
Results from a Seven Month Trial of Single Point Calibration
Geoffrey Rule - ARUP Laboratories

New Advances | Tuesday 3:00 PM Poster #58
Parallel Reaction Monitoring and Selected Reaction Monitoring Exhibit Comparable Quantitative Performance in Clinical Research and Forensic Applications
Xiaolei Xie - Thermo Fisher Scientific
New Advances | Tuesday 3:00 PM Poster #68  
**Meconium Targeted Drug Screening in 9 Seconds Per Sample Using Laser Diode Thermal Desorption Mass Spectrometry (LDTD-MS/MS)**  
*Pierre Picard* - Phytronix Technologies

New Advances | Wednesday 5:00 PM Poster #9  
**Improving the Detection of Thyroglobulin in Human Plasma for Clinical Research by Combining SISCAPA Enrichment and Microflow LC/MS**  
*Jay S. Johnson* - Waters Corporation

New Advances | Wednesday 5:00 PM Poster #51  
**A New Instrument that Combines Fast Microfluidic Separations with High Pressure Mass Spectrometry for Clinical Diagnostic Applications**  
*Christopher Brown* - 908 Devices

**Occupational and Environmental Health**

Occupational and Environmental Health | Tuesday 5:00 PM Poster #75  
**Exposure Biomarker Discovery for Toxic Phthalate Plasticizers Using Liquid Chromatography-High Resolution Mass Spectrometry and Metabolomics Approaches**  
*Pao-Chi Liao* - National Cheng Kung University

**Pain Management**

Pain Management | Monday 7:00 PM Poster #8  
**Improved Sample Preparation for the Analysis of 12 Opiates in Urine Using the Thomson eXtreme Filter Vials® by LC-MS/MS**  
*Dennis Peterson* - Thomson Instrument Company

Pain Management | Monday 7:00 PM Poster #26  
**Is Enantiomeric Testing of Methamphetamine Necessary?**  
*Nguyen Nguyen* - Soloniuk Pain Center

Pain Management | Monday 7:00 PM Poster #35  
**The Analysis of Common Antiepileptic Drugs in Human Urine by LC-MS/MS**  
*Susan Steinike* - Restek Corporation

Pain Management | Monday 7:00 PM Poster #65  
**Incorporating Analysis of Mitragynine into LC-ESI-MS/MS Methodology Routinely Used for Quantification of Pain Medication and Illicit Drugs in Urine**  
*Katherine Yahvah* - Kashi Clinical Laboratories

Pain Management | Monday 7:00 PM Poster #88  
**Direct Injection of Serum and Online Solid Phase Extraction for the Quantification of 35 Benzodiazepines and Metabolites by Liquid Chromatography MS/MS**  
*Valérie Thibert* - Thermo Fisher Scientific France

Pain Management | Tuesday 5:00 PM Poster #13  
**Validation of an Algorithm for Determining Urinary Medication Cutoffs Using Quantitative LC-MS/MS**  
*Amadeo Pesce* - UCSD

Pain Management | Tuesday 3:00 PM Poster #42  
**Pain Panel Drug Screening by Nanopost Array Laser Desorption Ionization Mass Spectrometry (NAPA LDI-MS) on REDIchip**  
*Christopher George* - Protea Biosciences, Inc.
Differential Recovery of Gabapentin and Pregabalin Utilizing SPE Extraction Demonstrated in a 42 Analyte Urine Confirmatory LC-MS/MS Panel

*Karsten Liegmann* - California State Polytechnic University, Pomona

A Multi-Class Drug and Metabolite Screen of 231 Analytes by LC-MS/MS

*Shane Stevens* - Restek Corporation

LC-MS/MS Method Development Challenges for the Separation of Non-Steroidal Anti-Inflammatory Drugs (NSAIDs)

*Frances Carroll* - Restek Corporation

Thyroid Hormone Analysis in NIST Standard Reference Materials

*Brittany Kassim* - National Institute of Standards and Technology

Harmonization in Individual Bile Acids Analysis in Mouse and Man – an Inter-Laboratory Ring Trial, Method Comparison and Clinical Relevance of Bile Acids

*Maria Chiam* - Biocrates Life Sciences AG

Peace of Mind in the Era of LDT Regulation - A Home-brew Barcoding Solution for Tracking Everything LC-MS/MS

*Krista Pratico* - UCSD Center for Advanced Laboratory Medicine

Improved Efficiency in Translation of Biomarker Development by Triple Component Human Serum Proteome Profiling for Diagnosis and Prognosis of Chronic Leukemia

*Yungkang Lee* - Berkshire Healthcare Systems

Development of Clinical Assays Based on Parallel Reaction Monitoring

*Bruno Domon* - Luxembourg Clinical Proteomics Center

Targeted LC-MS/MS Screening and Quantification of Proteins from Complex Biological Matrices Using a Retention Time Library in Place of Protein Standards

*Robert English* - Shimadzu Scientific Instruments

Quality Controls for the Quantification of Apolipoprotein L1 and Its Genetic Variants Based on Peptide Mass Spectrometry Measurements in Kidney Disease

*Dawn Z Chen* - Cedars-Sinai Medical Center

Proteomic Profiling Reveals Potential Novel Biomarkers of Aortic Stenosis in Affected Heart Tissue

*Anna Baud* - UCL Institute of Child Health

Calmodulin-Like Protein 5, a New Marker of Keratinocyte Differentiation, Disturbed in Atopic Eczema

*Emily Bliss* - UCL Institute of Child Health
Determination of Hemagglutinin Content in Influenza Vaccines Using Size Exclusion Chromatography and Quantitative Mass Spectrometry

Wanda Santana - Centers for Disease Control and Prevention

Tip-based Fractionation for Comprehensive Phosphoproteome Analysis

Alireza Dehghani - University of Bonn

Patients with Celiac Disease Display a Varying Oligoclonal Antibody Response to Tissue Transglutaminase: Characterization Utilizing a Proteomic Approach

Kari Gurtner - Mayo Clinic

Development of a Quantitative MS-based Assay for Intact BNP and Its Proteolytic Variants: Early Impressions with LC and CE from “High Flow” to “No-flow”

Koen Raedschelders - Cedars Sinai Medical Center

Continuing Development of BDX003 a Serum-based MALDI-TOF Test to Detect Hepatocellular Carcinoma in High-risk Patients

Nicholas Dupuis - Biodesix, Inc.

Comparison of Extraction Methods for the Quantification of Eculizumab from Serum Using Microflow LC-ESI-Q-TOF Mass Spectrometry

Paula Ladwig - Mayo Clinic

Quantitative Analysis of Protein Expression in Zebrafish Embryos Neuronally Expressing the Human EWSR1-ERG Oncogene

Dana Ohana - Leiden University Medical Centre

Multiplexed Quantification of a Serum Protein Panel to Monitor Treatment of Duchenne Muscular Dystrophy Patients

Linda Switzar - Leiden University Medical Center

Antibody-Independent SRM Strategies for Ultrasensitive and Multiplexed Quantification of Cancer Biomarker Candidates

Tujin Shi - Biological Sciences Division

Detection of UCN3 as a Biomarker for Obstructive Sleep Apnea in Children Using Multiple Reaction Monitoring

Tyler Yin - University of Louisville

A Multiplexed LC-MS/MS Method for Quantitative Analysis of Apolipoproteins in High-Density Lipoprotein

Robin Thomas - University of Minnesota

LC-MS/MS Measurements of Parathyroid Hormone-Related Protein (PTHrP): Negative Correlation Between Age and PTHrP Concentrations in CSF

Mark Kushnir - ARUP Institute
Proteomics | Tuesday 3:00 PM Poster #24
Characterizing Secreted Factors Contributing to Drug Resistance in Pancreatic Cancer Tumor Micro-Environment
Matthew Rosenow - Translational Genomics Research Institute

Proteomics | Tuesday 5:00 PM Poster #33
A Novel 6x5 Peptide Mixture for Full Instrument Characterization and Performance Monitoring
Michael Rosenblatt - Promega

Proteomics | Tuesday 3:00 PM Poster #52
New Approach for Intact Protein Separation, Detection, and Quantitation Based on Multiple Reaction Monitoring Triple Quadrupole Mass Spectrometry
Evelyn Wang - University of Texas at Arlington

Proteomics | Tuesday 5:00 PM Poster #55
Quantifying Translational Differences Between Single Blastomeres in the 16-cell Xenopus Embryo by Mass Spectrometry
Camille Lombard-Banek - The George Washington University

Proteomics | Tuesday 5:00 PM Poster #57
Development of a Sensitive, Accurate and Robust LC/MS-based Method for Profiling of Angiotensin Peptides in Plasma of Atherosclerotic ApoE-/-/LDLR-/- Mice
Mariola Olkowicz - Medical University of Gdansk

Proteomics | Tuesday 5:00 PM Poster #63
Quantitative LC-MS of Apolipoprotein L1 in Human Serum with High Throughput Automated Sample Preparation.
Shenyan Zhang - Cedars Sinai Medical Center

Proteomics | Tuesday 3:00 PM Poster #66
Quantification of Vitamin D-Binding Protein Isoforms by MRM
Lisa Kilpatrick - NIST

Proteomics | Wednesday 3:00 PM Poster #2
A Reference Measurement System for Urine Albumin
Ashley Beasley Green - NIST

Proteomics | Wednesday 5:00 PM Poster #3
Method Development of LC-MS Based Peptide Quantitation Assay to Differentiate Kininogen and Kallikrein Cleaved Kininogen
Gul Mustafa - Protea Biosciences, Inc.

Proteomics | Wednesday 3:00 PM Poster #8
LC/MS Analysis of Monoclonal Antibody Structure Utilizing HALO® BioClass Fused-Core™ Particles; Multilevel Analysis for Proteins and Glycovariants
Edward Faden - MAC-MOD Analytical

Proteomics | Wednesday 5:00 PM Poster #25
A Validated Amino Acid Analysis Assay for Accurate Quantification of Stable Isotope Labeled Thyroglobulin and Other Protein Reference Materials
Kevin Ray - MilliporeSigma

Proteomics | Wednesday 5:00 PM Poster #39
Preserving Specimen Integrity in Plasma Renin Activity Measurements
William O. Slade - LabCorp

Proteomics | Wednesday 5:00 PM Poster #49
Development and Validation of PreTRM™ - A Multi-Protein Predictor of Spontaneous Preterm Birth
Chad Bradford - Sera Prognostics, Inc.
Development of a Digested Yeast Protein Extract as a Mass Spectrometry Reference Material
Candice Johnson - National Institute for Standards and Technology

Diagnostic Protein Quantitation of 26 Actionable Targets in Patient Biopsies Using Clinical Mass Spectrometry
Wei-Li Liao - NantOomics, LLC

Applying a Proteoform Profiling Method for Neurological Disorder Biomarker Discovery
Nicolai Bache - Bruker Daltonics Inc.

Sample Prep & Automation

Effective Extraction Strategies for Buprenorphine and Norbuprenorphine in Urine, Oral Fluid and Whole Blood Using Cation Exchange Solid Phase Extraction and Sup
Elena Gairloch - Biotage

Matrix Effects Reduction with 2-D Online SPE-UHPLC-ESI-MS/MS for Trace Level Quantitation of Bisphenol A Analogues in Human Urine
Wei Zou - California Department of Public Health

Quick and Easy Sample Preparation of Urine for the Analysis of Psychoactive Drugs Using the Thomson eXtreme Filter Vials® by LC-MS/MS
Lisa Wanders - Technical Sales

A Fast and Effective Quantitation Method for Vitamin A & E from Human Serum Using Novum SLE in Conjunction with a Kinetex Evo C18 Column
Shahana Huq - Phenomenex

Generation of a Novel Digestion Protocol for Enhanced Proteome Coverage
Susan DiPietro - Thermo Fisher Scientific

Rapid Determination of Drug Protein Binding Affinity Using Solid Phase Micro Extraction
Craig Aurand - MilliporeSigma

Moving Towards the Standardization of Protein Quantification Workflows and Improving their Analytical Reproducibility
Mary Lame - Waters Corporation

Improved Speed & Reproducibility of Protein Digestion Using Novel Sample Preparation Technology
Sherry Gregory - Thermo Fisher Scientific

Determination of Urinary Opioids by Solid-Phase Extraction LC-MS/MS for Clinical Research: Comparison of Automated and Manual Sample Preparation
Teresa Pekol - Extend Consulting
Automated Desorption, SPE Extraction, and LC/MS/MS Analysis of Dried Blood Spots

Matthew Arnold - Gerstel, Inc.

A Novel Automated Sample Prep Process for an Improved LC/MS/MS 25-hydroxy Vitamin D Method

Joyce Flanagan - Marshfield Clinic

Cleanert HFMF® A New Sample Clean-up Technique for Plasma Sample Prior to LC-MS/MS in Bioanalysis

Warren Chen - Bonna-Agela Technologies

Fully Automated Broad Spectrum Extraction of Drugs and their Metabolites from Oral Fluid Samples Using Narrow Bore OFX Solid Phase Extraction Columns

David Hall - SPEware Corporation

Solid Phase Extraction Optimization and Separation of Vitamin D Metabolites by LC-MS/MS, for Clinical Research

Robert Wardle - Waters Corporation

Advances in Solid Phase Extraction – Removal of Residual Phospholipids Using a Novel Reverse-phase Sorbent

Jonathan Danaceau - Waters Corporation

Determination of PBDEs in Human Milk by Automated Solid Phase Extraction and Gas Chromatography/High Resolution Mass Spectrometry

Weihong Guo - California Department of Toxic Substances Control

In-line, Automated Method for the Sample Preparation and LC-MS/MS Analysis of Dried Matrix Blood Microsamples for Immunosuppressant Drug Monitoring

Erik Ruijters - MagnaMedics Diagnostics B.V.

Automated Comprehensive Urine Sample Preparation Using DPX Extraction on the Hamilton NIMBUS96 with LC-MS/MS Analysis

Kaylee Mastrianni - University of South Carolina

Multichannel Optimization of a New Four Channel HPLC with a Single Mass Spectrometer to Simplify Workflow Complexity and to Improve Throughput of LC-MS

Jason Lai - Thermo Fisher Scientific

Characterizing Matrix Depletion Using a Novel 96-well Format Extraction Media - Tecan® AC Extraction Plate™ (AC Plate).

Judy Stone - Univ. of Calif. San Diego Health System

Simple Extraction of Antidepressants from Whole Blood for LC-MS/MS Analysis Using Coated Well Plates

Dave van Staveren - Tecan Schweiz AG
Fast Determination of 17-Hydroxyprogesterone by LC-MS/MS for Diagnosis of Congenital Adrenal Hyperplasia

*Daniel Zhou* - Stanford Health Care

High Throughput Screening of Urine Marker Codes by Laser Ablation Electrospray Ionization Mass Spectrometry

*Callee Walsh* - Protea Biosciences

High-Throughput Preparation of Cellular FAMES and Sterols for GC/MS Analysis

*Kevin Williams* - University of California, Los Angeles

Exploring the Sources of Cross Contamination in 96-Well Sample Preparation Prior to LC-MS/MS Analysis

*Paul Roberts* - Biotage GB Limited

Catecholamine Analysis: Method Optimization to Improve Sensitivity and Reduce Limits of Quantitation Using LC-MS/MS

*Lee Williams* - Biotage GB Limited

Comparison of Sample Preparation Strategies for the Extraction of Methylmalonic Acid from Serum Prior to LC-MS/MS Analysis

*Rhys Jones* - Biotage GB Limited

All Roads Lead to Robots: Automation of Customized, Effective Trypsin Digestion

*Qin Fu* - Cedars Sinai Medical Center

Hydrolyze Your Way to Compliance – a Call for Pain Management Certified Reference Materials

*Heather Hochrein* - UC San Diego Health System

Automated, High Throughput Quantitative Analysis of 39 Drugs of Abuse in Oral Fluid Using DPX Extraction and LC-MS/MS

*William Brewer* - DPX Labs, LLC

Enhanced Recovery of Trypsin Digested Proteins Using Dispersive Pipette Extraction for Downstream Proteomic Analysis

*Yuzhe Nie* - University of South Carolina

Heat Stabilization Preserves the Molecular Integrity of the Sample

*Ylva Elias* - Denator AB


*Marta Kozak* - ThermoFisher Scientific

Integration of Steroids Analysis in Serum Using LC-MS/MS with Full-automated Sample Preparation

*Brian Feild* - Shimadzu Scientific Instruments
High Throughput Analysis for Novel Oral Anticoagulants Using LC-MS/MS System Integrated with Automated Sample Preparation
*Daisuke Kawakami* - Shimadzu Corporation

Comparison of Several Approaches for Vitamin D Metabolite Analysis
*Xuejun Zang* - Orochem Technologies, Inc.

The Novel LC-MS/MS System Integrated with Automated Sample Preparation for Drugs Analyses
*Hikaru Shibata* - Shimadzu Scientific Instruments, Inc.

A Novel Drug Screening Protocol for Acidic, Basic, and Neutral in Hydrolyzed Urine Using Supported Liquid Extraction Prior to LC-MS/MS Analysis
*Dan Menasco* - Biotage

Small Molecule Analytes

Improved Sensitivity for Immunosuppressant Monitoring in Two Dried Matrices: A Proof of Concept
*Jane Dickerson* - Seattle Children’s Hospital

Analysis of Flakka and Related Compounds by HILIC, Reversed-Phase and Chiral Chromatographic Modes
*David Bell* - MilliporeSigma

Sensitive and Specific LC-MS/MS Analysis of Methylmalonic Acid in Serum, Plasma and Urine
*Irene Doering* - RECIPE Chemicals + Instruments GmbH

Development and Validation of a Quantitative Method for Doxorubicin/Doxorubicinol in Serum and Saliva: Special Considerations for Working with Unstable Analytes
*Autumn Breaud* - The Johns Hopkins University

Quantitation of Serum Indoxyl Sulfate and P-Cresyl Sulfate in Chronic Kidney Disease by UPLC-MS/MS Method
*Chia-Ni Lin* - Chang Gung Memorial Hospital

Development and Validation of a LC-MS/MS Method for the Quantification of the Checkpoint Kinase 1 Inhibitor (CHK1) CCT245737 in Human Plasma
*Monique Zangarini* - Newcastle University

Effects of Nutrient Stress on Arginine and Dimethylarginine in Primary Hepatocytes
*Shu-Chu Shiesh* - National Cheng Kung University

Detecting THC Metabolites and Other Cannabinoids
*Toshi Ono* - Nacalai USA Inc.
Small Molecule Analytes | Monday 7:00 PM Poster #55
**A Sensitive Liquid Chromatography–Tandem Mass Spectrometry Method for the Simultaneous Determination of Serum Estradiol, Estrone, and Estriol**
*Feng Bai* - LABioMed at Harbor-UCLA Medical Center

Small Molecule Analytes | Monday 7:00 PM Poster #56
**Optimization of Derivatization Reaction Used in Sample Preparation Method in Analysis of Methylmalonic Acid in Plasma for Clinical Research**
*Mindy Gao* - Thermo Fisher Scientific

Small Molecule Analytes | Monday 7:00 PM Poster #57
**LCMS Based CSF Neurotransmitter Quantification for Following Psycho-pharmacotherapy in Psychiatric Disorders**
*Dimitri Brinet* - Sahlgrenka Academy at Gothenburg University

Small Molecule Analytes | Monday 7:00 PM Poster #68
**Development and Validation of LC-MS Based Autotaxin Functional Assay and Autotaxin Inhibitors Screening by PUF-LCMS**
*Yongchao Li* - University of Illinois at Chicago

Small Molecule Analytes | Monday 7:00 PM Poster #77
**Ionization Response of Stable Isotope Labeled Small Molecules and the Potential Impact on LC/MS/MS Assays**
*Sarah Aijaz* - Cerilliant Corporation

Small Molecule Analytes | Monday 7:00 PM Poster #82
**A UHPLC-MS/MS Method for Asymmetric Dimethyl Arginine (ADMA) a Prognostic Biomarker Among Patients with End-Stage Renal Disease**
*Amber Gray* - Mayo Clinic Foundation

Small Molecule Analytes | Tuesday 5:00 PM Poster #1
**Determination of Monosialogangliosides in Human Plasma by a Novel UPLC/MS/MS Assay in Combination with Chemical Derivatization**
*Qianyang Huang* - Cleveland State University

Small Molecule Analytes | Tuesday 3:00 PM Poster #6
**Simple and Cost-effective Generation of LC-MS/MS Interference Testing Materials**
*Richard King* - PharmaCadence Analytical Services

Small Molecule Analytes | Tuesday 3:00 PM Poster #26
**A Novel Integrated LC-MS/MS Strategy for the Ultra-sensitive Determination of Catecholamines in Human Peripheral Blood Mononuclear Cells (PBMC)**
*Xiaoguang (Sunny) Li* - Pharmasan Labs

Small Molecule Analytes | Tuesday 5:00 PM Poster #31
**Sensitive and Specific LC-MS/MS Analysis of Plasma Free Metanephrines Using Either On-line or Off-line Sample Cleanup**
*Katharina Kern* - RECIPE Chemicals + Instruments GmbH

Small Molecule Analytes | Tuesday 3:00 PM Poster #32
**Direct Injection of Serum and Online Solid Phase Extraction for the Quantification of Antidepressants by Liquid Chromatography Tandem Mass Spectrometry**
*Claudio De Nardi* - Thermo Fisher Scientific

Small Molecule Analytes | Tuesday 5:00 PM Poster #35
**A New Strategy for the Detection of the Family of Benzophenone-3 Structurally Related Compounds and their Metabolites in Human Urine Samples**
*Yu-Chen Chang* - California Department of Public Health
A Dilute-And-Shoot Method for Simultaneous Analysis of Vanillylmandelic Acid, Homovanillic Acid and 5-Hydroxyindoleacetic Acid in Human Urine

Shun-Hsin Liang - Restek Corporation

Determination of Asymmetric Dimethylarginine (ADMA) and Symmetric Dimethylarginine (SDMA) in Human Serum by Ion-Pair Chromatography-Mass Spectrometry

Haiqing Ding - Cleveland HeartLab, Inc.

Simultaneous Therapeutic Drug Monitoring for Voriconazole, Posaconazole, Fluconazole, Itraconazole, and Metabolites in Human Serum by HPLC-MS/MS

Yi Xiao - Children's Hospital Los Angeles

Bioanalytical UPLC-MS/MS Method Development and Validation for Measuring Most Commonly Used Antimicrobials in England from Human Blood Plasma

Karin Kipper - St. George’s, University of London

Development of Reference Measurement Procedure for 24R,25-Dihydroxyvitamin D3 and Value Assignment on SRMs of Vitamin D Metabolites in Human Serum

Susan Tai - National Institute of Standards and Technology

Evaluation of a New Four-Channel LC and a Mass Spectrometer for Open-Access Analysis of Multiple Drug Classes in Clinical Research

Kristine Van Natta - Thermo Fisher Scientific

Simultaneous Analysis of Nineteen Amino Acids in HuangQi Injection Using AQC Pre-column Derivatization and UPLC/Q-tof-MS

Su Zhang - California Department of Public Health

A Liquid Chromatography-tandem Mass Spectrometry Method for the Detection of Beta-carotene in Serum

Jessica Gifford - Calgary Laboratory Services

Performance Evaluation of the Multiplex Assays for First-line Anti-tuberculosis Drugs in Dried Blood Spots Using UPLC–MS/MS

Kyunghoon Lee - Seoul National University Hospital

Quantitation of 22 Long Chain Fatty Acids by GC-NCl-MS in Serum and Plasma

Erik Kish-Trier - ARUP Laboratories

Ultra Performance Liquid Chromatography-Tandem Mass Spectrometry Determination of Tryptophan and Its Kynurenine Metabolites

Li Wang - BC Children’s Hospital

Use of the HemaSpot HF™ Blood Collection Device to Monitor Cortisol Chronobiology

Jeanette Hill - Spot On Sciences
Small Molecule Analytes | Wednesday 5:00 PM Poster #63
**Analyte Stability from Dried Blood Collected on HemaSpot-HF™ Devices**
*James Hill* - *Spot On Sciences, Inc.*

Small Molecule Analytes | Wednesday 3:00 PM Poster #68
**Ultra-Fast Quantification of Antidepressants in Urine at 9 Seconds Per Sample Using LDTD-MS/MS**
*Alex Birsan* - *Phytronix Technologies*

Small Molecule Analytes | Wednesday 5:00 PM Poster #71
**High Throughput Quantitation for Therapeutic Drug Monitoring with Open Access LC/MS/MS System**
*Miho Kawashima* - *Shimadzu Corporation*

Small Molecule Analytes | Wednesday 3:00 PM Poster #74
**Fast Analysis of Low pg/mL Level Testosterone in Serum by Bruker TQ LC/MS**
*Zicheng Yang* - *Bruker Daltonics*

### Tissue Imaging & Analysis

Tissue Imaging & Analysis | Monday 7:00 PM Poster #1
**Direct Correlation of Cytological Specimens and Lipids with Morphologically Compatible Ambient Pressure Ionization Mass Spectrometry**
*Matthew Olson* - *Johns Hopkins University School of Medicine*

Tissue Imaging & Analysis | Monday 7:00 PM Poster #58
**Structure Specific Immunolabeling and Mass Spectrometric Probing of Amyloid Beta Plaque Pathology in Alzheimer’s Disease**
*Wojciech Michno* - *Sahlgrensk Academy at the University of Gothenburg*

Tissue Imaging & Analysis | Monday 7:00 PM Poster #59
**Polarity Switching Mass Spectrometry Imaging of Healthy and Cancerous Hen Ovarian Tissue Sections by IR-MALDESI**
*Milad Nazari* - *North Carolina State University*

Tissue Imaging & Analysis | Monday 7:00 PM Poster #61
**Rapid Evaporative Ionisation Mass Spectrometry (REIMS) in Endoscopy: Preparing for Clinical Translation**
*James Alexander* - *Imperial College, London*

Tissue Imaging & Analysis | Monday 7:00 PM Poster #66
**Ambient Mass Spectrometry Imaging for Assessing P53 Mutation Status in Breast Cancer**
*Jialing Zhang* - *UT Austin*

Tissue Imaging & Analysis | Monday 7:00 PM Poster #80
**Translational Bioinformatics for Mass Spectrometry Imaging in a Clinical Research Setting**
*Bindesh Shrestha* - *Waters Corporation*

Tissue Imaging & Analysis | Tuesday 5:00 PM Poster #3
**DESI-imaging: Histology Applications**
*Renata Soares* - *Imperial College London*

Tissue Imaging & Analysis | Tuesday 3:00 PM Poster #10
**Targeted Protein Quantification from FFPE Tumor Tissue Using Mesodissection and Liquid Tissue SRM Assay: Comparison to a Laser Microdissection Platform**
*Chao Gong* - *NantOmics*

Tissue Imaging & Analysis | Tuesday 5:00 PM Poster #29
**Multi-Modal Mass Spectrometry Imaging for Clinical and Biomedical Research Applications – a Comparison of MALDI and DESI Techniques for Tissue Imaging**
*Emanuelle Claude* - *Waters Corporation*
Tissue Imaging & Analysis | Tuesday 3:00 PM Poster #50
Mass Spectrometry Imaging of Biological Tissue Sections and Small Cell Clusters on Nanophotonic Laser Desorption Ionization Substrates
Sylwia Stopka - The George Washington University

Tissue Imaging & Analysis | Tuesday 5:00 PM Poster #59
Quantitative Mass Spectrometry Imaging of Chemotherapeutics in Tissue Sections Using IR-MALDESI
Mark Bokhart - North Carolina State University

Tissue Imaging & Analysis | Tuesday 5:00 PM Poster #81
Phospholipids as Potential Biomarkers for Ovarian Cancer: Spatial Localization and Use in Diagnosis
Luisa Doria - Imperial College London

Tissue Imaging & Analysis | Wednesday 3:00 PM Poster #10
Improving Biochemical Content - Discriminating Lipid and Metabolite Distribution Using DESI and High Resolution Mass Spectrometry in Healthy and Diseased Tissue
Joseph Kennedy - Prosolia, Inc.

Tissue Imaging & Analysis | Wednesday 5:00 PM Poster #43
Quantitative Imaging of Platinum Based on Laser Ablation-inductively Coupled Plasma-mass Spectrometry to Investigate Toxic Side Effects of Cisplatin
Tom Weaver - Teledyne CETAC Technologies

Tissue Imaging & Analysis | Wednesday 3:00 PM Poster #64
Automated Tumor Typing of Tissue Sections Based on MALDI Mass Spectrometry Imaging Data and Machine Learning Using Characteristic Spectral Patterns
Tobia Boskamp - University of Bremen

Toxicology

Toxicology | Monday 7:00 PM Poster #4
Efficient Forensic Toxicological Screening and Quantitation Workflow Using QTOF LC-MS/MS System
Jenny Moshin - SCIEX

Toxicology | Monday 7:00 PM Poster #23
Rapid, Simplified and Highly Efficient Analysis of Urinary THC and Metabolites Using a Novel Reversed-phase Extraction Sorbent
Kim Haynes - Waters Corporation

Toxicology | Monday 7:00 PM Poster #29
Analysis of a Toxicology Panel Using High-efficiency Cortecs Phenyl Columns
Arnie Aistars - Waters Corporation

Toxicology | Monday 7:00 PM Poster #33
An Investigation into Removing the Excipients from Select Oral Fluids Collection Devices by SPE and LC/MS Detection
Seyed Sadjadi - Phenomenex, Inc.

Toxicology | Monday 7:00 PM Poster #51
The Application of DPX WAX Tips in Clinical Toxicology for Protein Precipitation
William Kemnitzer - DPX Labs

Toxicology | Monday 7:00 PM Poster #52
Method Validation for Nicotine and Its Metabolites by LC-MSMS Reveals a Low Clinical Utility for the Tobacco Alkaloid Anabasine
Matthew Feldhammer - Emory University
Toxicology | Monday 7:00 PM Poster #67
**LC-MS/MS Analysis of 25 Opioids from Dried Urine Spots**  
Jessica Boyd - Calgary Laboratory Services/University of Calgary

Toxicology | Monday 7:00 PM Poster #75
**Point-of-care Identification of Ingested Intoxicants by Thermal Desorption Electrospray Ionization/Mass Spectrometry in the Emergency Room**  
Chi-Wei Lee - Kaohsiung Medical University

Toxicology | Monday 7:00 PM Poster #76
**LDTD-MS/MS Method for Quantitative Analysis of Four Immunosuppressant Drugs in Whole Blood and Cost Analysis Comparison to LC-MS/MS**  
Stephen Merrigan - ARUP Institute for Clinical and Experimental Path

Toxicology | Monday 7:00 PM Poster #79
**Amphetamine- and Methamphetamine-like Compounds Identified in Urine from an Over-The-Counter Dietary Supplement**  
Justin Wotring - InSource Diagnostics

Toxicology | Tuesday 5:00 PM Poster #11
**Rapid and Sensitive Analysis of a 93-Compound Forensic Panel in Urine**  
Xiang He - SCIEX

Toxicology | Tuesday 5:00 PM Poster #15
**Utility of Suspect Screening by High Resolution Mass Spectrometry: Adulterated Xanax**  
Xander van Wijk - University of California, San Francisco

Toxicology | Tuesday 3:00 PM Poster #44
**An Ion Mobility Screening Approach for the Detection of Toxicologically Relevant Substances**  
Jeff Goshawk - Waters Corporation

Toxicology | Tuesday 3:00 PM Poster #76
**Evaluation of Lab Developed Test for Simultaneous Determination of Sirolimus and Everolimus by Liquid Chromatography Tandem Mass Spectrometry**  
Seungman Park - GreenCross Laboratories

Toxicology | Tuesday 3:00 PM Poster #78
**Qualitative Analysis for Multiple Drugs in Urine by Liquid Chromatography Time-Of-Flight Mass Spectrometry (LC-TOF/MS)**  
Kathryn Smith - ARUP Laboratories

Toxicology | Tuesday 5:00 PM Poster #85
**A Coupled Analysis of Low and High Abundance Isotopes Extending the Dynamic Range of an Assay for Methamphetamine in Meconium via LC-MSMS**  
Melissa Goggin - MEDTOX Laboratories

Toxicology | Wednesday 3:00 PM Poster #6
**Immunosuppressant (Tacrolimus/Cyclosporin A) Monitoring by LC-MS/MS Using Mitra Microsampling Devices**  
Michael Mbughuni - Mayo Clinic

Toxicology | Wednesday 5:00 PM Poster #7
**Cost Effective Dilute-and-shoot Approach for Determination of Illicit Drugs in Oral Fluids Using LC-MS/MS**  
Kavinda De Silva - MTL

Toxicology | Wednesday 5:00 PM Poster #15
**Toxicology Testing in Complex Patient Populations Requires Definitive Testing**  
Emily Ryan - LabSource, LLC
Unified Drug Testing by Online SPE-LC/MS/MS for High Productivity & Ease of Use: One Totally Automated Method Measures ALL Drugs in Urine & Oral Fluids

Mark Hayward - ITSP Solutions

Enzyme Hydrolysis of Haloperidol Glucuronide; a Major Urine Metabolite of Haldol®

Gregory McIntire - Ameritox, LTD

Translational Mass Spec

Molecular Basis for Polycystin-2 Channel Regulation and Assembly via Its C-terminal Tail

Yifei Yang - Yale University

Rapid Evaporative Ionization Mass Spectrometry During Brain Surgery: Our Experience of Real-Time Intraoperative Tumour Characterisation

Babar Vaqas - Imperial College, London

Quantitative Analysis of Human Tear Fluid by MALDI-TOF Mass Spectrometry

Ryan Walsh - University of Colorado, Denver (AMC)

Detection of Lyme Disease Infection Through Quantification of Borrelia burgdorferi Membrane Proteins

Karen Phinney - National Institute of Standards and Technology

Investigating the Lipidomic Profile Derived Through Rapid Evaporative Ionisation Mass Spectrometry of Breast Tissue Samples

Merja Rossi - Imperial College, London

Development of a Routine Hemoglobin Profiling Workflow

Scott Peterman - Thermo Fisher Scientific

The Role of UHPLC-MS/MS in Preclinical and Clinical Studies of Drug Interactions with Botanical Dietary Supplements

Richard van Breemen - University of Illinois College of Pharmacy

Translational Research Workflows on LC-HRAM Platform for Detection of Pathogen Induced Cancer in Human T-Cell Leukemia Virus Type 1 Disease

Sucharita Dutta - EVMS

A Split Hair Comparison of Human Hair Cortisol Levels Using an Immunoassay versus Liquid Chromatography-Mass Spectrometry

Howard Horng - University of California, San Francisco

Targeted SPE-UPLC-MS/MS Analysis of Oxylipins: from Profiling to Quantification for Translational Research Studies

Billy Molloy - Waters Corporation
Successful Implementation of Immunosuppressant Drugs (ISDs) Monitoring Using Liquid Chromatography Mass Spectrometry (LC-MS/MS)
Xiaowei Fu - Children's Hospital Los Angeles

Utilizing Western Blot and Mass Spectrometry to Improve Immunohistochemical Detection of Predictive Biomarkers in a Clinical Setting
Heather O’Neill - Caris Life Sciences

Application of Microfluidic Tandem Quadrupole LC-MRM-MS Based Translational Research Analysis of Putative Heart Failure Peptide Biomarkers in Human Plasma
Khalid Khan - Waters Corporation

Development of a Rapid LC-MS/MS Method for Human Serum Lipid Mediator Profiling
Ben Figard - Shimadzu Scientific Instruments

Judging a Book by Its Data: Planning Experiments to Fully Evaluate Prospective Instrument Vendors
Thomas Laha - University of Washington

Identification of Two Frequent Hemoglobin Variants in Korea by Liquid Chromatography – Tandem Mass Spectrometry
Seung Jun Lee - Seoul National University Hospital

Use of an Animal-free Synthetic Surrogate Serum Matrix for Assay Calibrators, Controls, and Patient Sample Diluent in ELISA and LC-MS Based Clinical Assays
Jim Walters - MilliporeSigma
Monday 7:00 PM
Poster #1 in Exhibit Hall
Direct Correlation of Cytological Specimens and Lipids with Morphologically Compatible Ambient Pressure Ionization Mass Spectrometry
Matthew Olson - Johns Hopkins University School of Medicine (molson8@jhu.edu)

Cytological specimens are among the most abundant in anatomic pathology services worldwide because they are obtained through non- and minimally invasive methods. However, cytology challenges pathologists because limited sampling strategies are so appealing to clinicians and patients are small. Thus, the cytologic diagnostic process is amenable to ancillary testing, especially when it does not interfere with classical morphology. Herein we present an ambient pressure ionization technique validated for both morphology and mass spectrometric analysis and compatible with routine cytological processing. We also demonstrate the need to choose a preservative that is amenable both to morphological and mass spectrometric analyses.

Monday 7:00 PM
Poster #2 in Exhibit Hall
Accuracy Evaluation of Routine Vitamin D Immunoassays Compared with LC-MS/MS in Pregnant Women and Intensive Care Unit Patients
Yeo-Min Yun - Konkuk University School of Medicine (ymyun@kuh.ac.kr)

Serum samples of 160 healthy controls, 50 pregnant women, and 50 intensive care unit (ICU) patients were collected. Total 25(OH)D levels of each sample were measured by LC-MS/MS and three automated assays, including ADVIA Centaur (Siemens, Germany), Elecsys (Roche, Switzerland), and Architect i200SR (Abbott, US). The vitamin D results of all three routine immunoassays showed poor concordance compared with those of LC-MS/MS in ICU patients than those in healthy controls. In pregnant women, the vitamin D results of ADVIA Centaur showed the high positive bias compared with vitamin D values measured by LC-MS/MS. In conclusion, standardization of each immunoassays is essential for clinical use to estimate vitamin D status. Moreover, for the exact vitamin D status evaluation in ICU patients and pregnant women, using LC-MS/MS measurement would be recommended.

Monday 7:00 PM
Poster #3 in Exhibit Hall
Quantification of Testosterone in Serum by Liquid Chromatography-tandem Mass Spectrometry
Vasanta Putluri - Baylor College of Medicine (vputluri@bcm.edu) -- *Young Investigator Grantee*

Androgens (such as testosterone) are natural hormones. They are important in sexual development in both men and women. In women, androgens are produced in small amounts by the ovaries and the adrenal glands. Similar to higher blood estrogen levels, higher amounts of androgens in the blood may be linked to an increased risk of breast cancer in women. An ultra sensitive quantitative analytical method is required for total testosterone in human serum to be able to measure the low levels found in women. Therefore, a method was developed on an Agilent 6495 Ion Funnel Mass Spectrometer to quantify and characterize testosterone underivatized in serum and to ascertain which method may be the most appropriate for laboratory use.

Monday 7:00 PM
Poster #4 in Exhibit Hall
Efficient Forensic Toxicological Screening and Quantitation Workflow Using QTOF LC-MS/MS System
Jenny Moshin - SCIEX (Jenny.Moshin@sciex.com)

Quadrupole Time-of-Flight (QTOF) mass spectrometry is becoming the desired technology for sensitive and selective screening workflows in a forensic toxicological setting. It affords accurate mass and mass resolution capabilities combined with sensitivity as well as the capability to perform simultaneous highly specific targeted quantification and non-targeted screening and the ability to perform retrospective data mining. Here we describe a new QTOF system with intuitive new software for easy adoption of accurate mass technology to forensic testing. In this paper we demonstrate that the new hardware and software combined allow the highest level of confidence for compound identification and quantification from blood and urine samples.
Monday 7:00 PM
Poster #5 in Exhibit Hall
**Effective Extraction Strategies for Buprenorphine and Norbuprenorphine in Urine, Oral Fluid and Whole Blood Using Cation Exchange Solid Phase Extraction and Sup**

*Elena Gairloch* - *Biotage* (elena.gairloch@biotage.com)

Introduction: Buprenorphine and Norbuprenorphine are typically problematic for analysis due to analyte stability issues during sample preparation. A fast and robust testing protocol is needed to address extracting the targets out of complex matrices typically encountered during toxicological testing. The sample preparation method would also be expected to yield good analyte recovery and minimum matrix effects. Here, we demonstrate new rapid and reliable sample preparation methods that were used to extract the target analytes from small amounts of complex biological matrix. Qualitative and quantitative data demonstrates the utility of these methods prior to LC-MS/MS analysis.

Monday 7:00 PM
Poster #6 in Exhibit Hall
**Development and Validation of LC-MS/MS Method for Determination of Testosterone in Serum**

*Eun Hee Lee* - *Green Cross Laboratories* (eunice7879@gmail.com)

We developed liquid chromatography-tandem mass spectrometry (LC-MS/MS) method for serum total testosterone. The accuracy, imprecision, limit of quantification (LOQ), and linearity of LC-MS/MS method were validated and compared with enzyme chemiluminescence immunoassay (ECLIA) and radioimmunoassay (RIA) methods. The accuracy, precision, LOQ, and linearity were excellent. Especially the accuracy for LC-MS/MS method was better than ECLIA and RIA methods. The LC-MS/MS method showed excellent performance compared with ECLIA and RIA.

Monday 7:00 PM
Poster #7 in Exhibit Hall
**Improved Efficiency in Translation of Biomarker Development by Triple Component Human Serum Proteome Profiling for Diagnosis and Prognosis of Chronic Leukemia**

*Yungkang Lee* - *Berkshire Healthcare Systems* (hugolee@alumni.usc.edu) -- *Young Investigator Grantee*

Successful translation during biomarker development with complex human serum proteome requires ultra-high resolution protein identification technologies. Here we devised a triple component serum proteome profiling method that integrated serum abundant protein depletion, MudPIT, and segment survey scan mass screening, by which its effectiveness to increasing peptide and protein coverages as well as run-to-run reproducibility at very low false discovery rate was studied, comparing to one-dimension shotgun proteomic approach. We further applied this method to biomarker development for diagnosis and prognosis of chronic myelogenous leukemia and chronic lymphocytic leukemia, due to the facts that clinical symptoms of chronic leukemia are often non-specific where the American Cancer Society estimates that at least one-fifth of the people with leukemia have been underdiagnosed.

Monday 7:00 PM
Poster #8 in Exhibit Hall
**Improved Sample Preparation for the Analysis of 12 Opiates in Urine Using the Thomson eXtreme Filter Vials® by LC-MS/MS**

*Dennis Peterson* - *Thomson Instrument Company* (dennis.peterson@htslabs.com)

This improved sample preparation method allows for the quantitative measurement of opiates in urine. The urine samples were prepared using the eXtreme|FV®, followed by LC/MS/MS analysis. The most critical aspects of reliable urine analysis are the reduction of interferences from the sample matrix and analyte recovery. eXtreme|FV®, were compared to an existing SPE sample preparation method to reduce the sample matrix causing interference prior to analysis. SPE is time consuming, adversely impacts recovery, uses large amounts of solvent and are expensive. The improved sample preparation method using the Thomson eXtreme|FV® allows for the analysis of 12 Opiates.
Monday 7:00 PM
Poster #9 in Exhibit Hall
Matrix Effects Reduction with 2-D Online SPE-UHPLC-ESI-MS/MS for Trace Level Quantitation of Bisphenol A Analogues in Human Urine
Wei Zou - California Department of Public Health (WEI.ZOU@CDPH.CA.GOV)
- In the current study, a 2-D online SPE method has been developed to reduce matrix effects, and therefore, to improve limit of detection (LOD). We found out that the second dimension SPE helped to reduce the matrix effects significantly.

Monday 7:00 PM
Poster #10 in Exhibit Hall
Quick and Easy Sample Preparation of Urine for the Analysis of Psychoactive Drugs Using the Thomson eXtreme Filter Vials® by LC-MS/MS
Lisa Wanders - Technical Sales (lisa.wanders@htslabs.com)
- This improved sample preparation method allows for the quantitative measurement of psychoactive drugs, Benzodiazepines in urine. The urine samples were prepared using the eXtreme|FV®, followed by LC/MS/MS analysis. The most critical aspects of reliable urine analysis are the reduction of interferences from the sample matrix and analyte recovery. eXtreme|FV®, were compared to SPE for sample preparation to reduce the sample matrix causing interference prior to analysis. SPE is time consuming, adversely impacts recovery, uses large amounts of solvent and are expensive. The improved sample preparation method using the Thomson eXtreme|FV® allows for the analysis of 9 Benzodiazepines.

Monday 7:00 PM
Poster #11 in Exhibit Hall
Improved Sensitivity for Immunosuppressant Monitoring in Two Dried Matrices: A Proof of Concept
Jane Dickerson - Seattle Children’s Hospital (jane.dickerson@seattlechildrens.org)
- We aim to improve the clinical utility of remote collection of dried blood spots (DBS) for immunosuppressant monitoring with an enhanced method requiring less blood in both DBS and Mitra blood collection device. Immunosuppressants were quantified using deuterated internal standards on SCIEX QTRAP 6500. Limits of detection and quantitation were determined, with similar results using 3-mm DBS (3 µL) and Mitra device (10 µL). The method correlated well with previously published method using 8-mm DBS extractions. We believe this new method will eliminate the majority of rejected samples due to QNS and allow more families to participate in the remote monitoring program.

Monday 7:00 PM
Poster #12 in Exhibit Hall
A Fast and Effective Quantitation Method for Vitamin A & E from Human Serum Using Novum SLE in Conjunction with a Kinetex Evo C18 Column
Shahana Huq - Phenomenex (shahanaH@phenomenex.com)
- Nutritional supplements like vitamins and minerals are critical measure of a patients overall health condition that underwent a gastric bypass and other types of bariatric surgery. In order to quantify the nutritional intake of a patient, we have developed a simple and reliable method to extract vitamin A & E from human serum, using Novum SLE. A Kinetex 5u, Evo C18, 100x2.1 mm HPLC column was utilized to obtain the best selectivity of the two vitamer of vitamin E, alpha and gamma tocopherol along with vitamin A, while a polarity switching technique in mass spectrometric ionization was employed.

Monday 7:00 PM
Poster #13 in Exhibit Hall
Generation of a Novel Digestion Protocol for Enhanced Proteome Coverage
Susan DiPietro - Thermo Fisher Scientific (susan.dipietro@thermofisher.com)
- Identification and quantification of biomarkers is often hindered by poor sample solubility and incomplete protein digestion. Clean-up and enrichment strategies can improve analytical sensitivity, however these approaches cannot enhance the rate of trypsin digestion or its reproducibility. A novel digestion technique has been developed to overcome these barriers by increasing the efficiency and reproducibility of digestion, whilst significantly improving the workflow efficiency.
Monday 7:00 PM
Poster #14 in Exhibit Hall
**Development of Clinical Assays Based on Parallel Reaction Monitoring**

*Bruno Domon* - *Luxembourg Clinical Proteomics Center* (bruno.domon@lih.lu)

Targeted proteomics analyses of biomarkers are routinely performed on triple quadrupole mass spectrometers, which present limited selectivity. The analyses of clinical samples performed on a quadrupole-orbitrap instrument using parallel reaction monitoring (PRM) showed a significant gain in sensitivity and selectivity. A new acquisition method leveraging the presence of internal standards showed a dramatic improvement of the reliability and the precision of the analyses. The method has a broad applicability to the quantitative analysis of clinical samples, such as lung cancer plasma samples to discriminate the disease stages and subtypes, and of tissue samples to map driver mutations (EGFR and KRAS).

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Monday 7:00 PM
Poster #15 in Exhibit Hall
**Targeted LC-MS/MS Screening and Quantification of Proteins from Complex Biological Matrices Using a Retention Time Library in Place of Protein Standards**

*Robert English* - *Shimadzu Scientific Instruments* (rdenglish@shimadzu.com)

LC-MS/MS is a robust platform for quantifying targeted proteins in complex matrices. Typically, quantitative protein assays are developed using comparable synthetic or expressed protein standards to establish method conditions appropriate for measurement of clinical samples. Here a mixture of common proteins was used to develop a retention time library for a set UHPLC method, which Skyline utilized to estimate peptide retention times as well as MRM transitions and instrument parameters from known sequences effected in chicken plasma by Salmonella endotoxins. Utilizing key instrument and software capabilities, a targeted method was quickly developed without the use of comparable standards.

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Monday 7:00 PM
Poster #16 in Exhibit Hall
**Quality Controls for the Quantification of Apolipoprotein L1 and Its Genetic Variants Based on Peptide Mass Spectrometry Measurements in Kidney Disease**

*Dawn Z Chen* - *Cedars-Sinai Medical Center* (chenzh@cshs.org) -- *Young Investigator Grantee*

In the translation of building a clinical LC-MS/MS assay on MRM peptides in compliance with high throughput for patients, the initial small-scale experiments have to demonstrate the traceability along the workflow. Apolipoprotein L1 (ApoL1), an HDL lipoprotein with three genetic variants, is used as a model protein to assess the strategies of standards, matrix effects, and the quality controls for the enzymatic digestion. A simple, high-throughput, quantitative LC-MS/MS ApoL1 assay has been successfully developed, validated and then applied to 235 participants to examine the associations between chronic kidney disease with ApoL1 plasma levels and its genetic variants.

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Monday 7:00 PM
Poster #17 in Exhibit Hall
**High Serum Lipids Cause Erroneously Low Total 25-OH Vitamin D Levels by a Chemiluminescent Immunoassay.**

*Joshua Hayden* - *Weill Cornell Medical College* (jah9108@med.cornell.edu)

The DiaSorin Liaison® chemiluminescent immunoassay (CIA) for total 25-OH vitamin D (25-OH vit D) has begun to replace mass spectrometry as the method of choice in many clinical laboratories. This work examined the performance of this assay in routine clinical practice. A total of 153 paired samples were analyzed by the CIA and an in-house tandem mass spectrometry assay. While the DiaSorin showed acceptable performance overall, substantial negative bias was observed in samples with elevated lipids (total cholesterol, triglycerides and high density lipoprotein (HDL)); mixing studies confirmed the CIA underestimates 25-OH vit D levels in samples with elevated cholesterol. Clinical laboratorians should be aware that the CIA can yield erroneously low 25-OH vit D levels in the presence of elevated lipids.
Proteomic Profiling Reveals Potential Novel Biomarkers of Aortic Stenosis in Affected Heart Tissue

Anna Baud - UCL Institute of Child Health (a.baud@ucl.ac.uk)

- Aortic stenosis (AS), the most common form of valve disease in the Western world, occurs due to progressive narrowing of the aortic valve (AV) orifice, resulting in slowly increasing load onto the left ventricle (LV). The LV responds with a myriad of adaptive changes, which eventually become maladaptive. Current management is focused on assessing the severity of valve stenosis, but neglects the myocardial response, that is pivotal for timing of surgery and prognosis. The aim of this pilot study is to find new biomarkers of myocardial remodeling that could refine our understanding of maladaptive changes in aortic stenosis and ultimately allow to optimize the timing of surgery.

Calmodulin-Like Protein 5, a New Marker of Keratinocyte Differentiation, Disturbed in Atopic Eczema

Emily Bliss - UCL Institute of Child Health (emily.bliss.10@ucl.ac.uk) -- *Young Investigator Grantee*

- Atopic eczema is a skin disease that affects approximately 25% of children and between 1 and 3% of the adult population in the UK. In atopic eczema the skin barrier is disturbed to the extent that it no longer functions to retain as much water as usual, resulting in an itchy, red skin rash. Label free proteomics was used to identify protein markers that may potentially be able to elucidate the mechanism behind this change. Fourteen proteins we identified as being significantly changed between control and atopic eczema elbow scrapings were selected for validation by immunohistochemical staining. Alpha-1 acid glycoprotein, bleomycin hydrolase, calmodulin-like protein 3, cathepsin D and dermcidin all showed changes, however calmodulin–like protein 5 was the most significant.

Evaluation of Measurement for Serum 3-epi-25-hydroxyvitamin D3, 25-hydroxyvitamin D3 and 25-hydroxyvitamin D2 Using UPLC-MS/MS in a Korean Reference Laboratory

Sung Eun Cho - LabGenomics Clinical Laboratories (secho0824@gmail.com)

- We evaluated the performance of Ultra-Performance Liquid Chromatography Tandem Mass Spectrometry (UPLC-MS/MS) method to measure serum 3-epi-25-hydroxyvitamin D3 (epi-25(OH)D3), 25-hydroxyvitamin D3 (25(OH)D3) and 25-hydroxyvitamin D2 (25(OH)D2). Using Kinetex XB-C18 column (Phenomenex, USA) and isocratic methanol/water (77.5/22.5, v/v) flowing at 0.25 mL/min, run time was 13 minutes/sample. TQD triple quadrupole mass spectrometer (Waters, USA) with MRM transitions, MSMS Vitamin D kit (PerkinElmer, Finland) and PTAD derivatization method were used. Intra- and inter-run precisions were less than 15 %. The carryover was 0.10%, -0.27% and 0.10%, respectively. There was no ion suppression. The linearity was good with $R^2>0.9999$. The peak of epi-25(OH)D3 was clearly separated from that of 25(OH)D3 in the XIC. The performance of UPLC-MS/MS for epi-25(OH)D3, 25(OH)D3, and 25(OH)D2 was acceptable.

Determination of Hemagglutinin Content in Influenza Vaccines Using Size Exclusion Chromatography and Quantitative Mass Spectrometry

Wanda Santana - Centers for Disease Control and Prevention (wsantana@cdc.gov)

- Size exclusion chromatography (SEC) has been employed to separate HA species under the same conditions employed in the SRID assay. In order to determine the amount of the active form of HA in the vaccine, we have used a protocol where vaccine samples are first separated by SEC followed by LC-MS/MS quantitation of the protein components. The same SEC fractions may also be subject to SRID analysis to determine the fractions with SRID activity. A measure of potency can be calculated by summing the concentrations of all fractions that are SRID active. We have also demonstrated that the SRID active fractions can reproducibly be isolated via size exclusion chromatography and that the assay is also stability indicating, based on changes observed in the SEC profile of vaccines subjected to pH based stress.
**Monday 7:00 PM**  
**Poster #23 in Exhibit Hall**  
**Rapid, Simplified and Highly Efficient Analysis of Urinary THC and Metabolites Using a Novel Reversed-phase Extraction Sorbent**  
*Kim Haynes - Waters Corporation (kim_haynes@waters.com)*  
- A novel reversed-phase SPE sorbent has been used to rapidly analyze urinary THC and its major metabolites. Extraction of pretreated samples was rapid and UPLC/MS/MS analysis was complete in less than 3 minutes. Extraction recoveries were efficient and consistent, and matrix effects were minimal. All quantitative parameters such as linearity, accuracy, and precision were well within established limits for bioanalytical and forensic methods. This method represents a simplified and highly efficient approach for the analysis of these important compounds.

**Monday 7:00 PM**  
**Poster #24 in Exhibit Hall**  
**Rapid Determination of Drug Protein Binding Affinity Using Solid Phase Micro Extraction**  
*Craig Aurand - MilliporeSigma (craig.aurand@sial.com)*  
- In this study, a novel BioSPME micro extraction device is evaluated as a rapid means of determining drug protein binding affinities from plasma. Here, a model set of drugs with varied range of protein binding affinities were utilized to evaluate the utility of the BioSPME sampling technique. Initial studies demonstrate that drug binding affinities can be determined in less than 30 minutes using the micro extraction technique.

**Monday 7:00 PM**  
**Poster #25 in Exhibit Hall**  
**Analysis of Flakka and Related Compounds by HILIC, Reversed-Phase and Chiral Chromatographic Modes**  
*David Bell - MilliporeSigma (dave.bell@sial.com)*  
- In this study liquid chromatography coupled to mass spectrometry (LC/MS) was applied to develop a method or set of methods that could be utilized for the analysis of Flakka and related compounds in biological fluids. HILIC, RPLC and chiral liquid chromatography were explored. Suitable conditions were obtained in each of the modes using a variety of stationary phase and mobile phase combinations. In addition to the general analysis, chiral conditions were also developed to separate the enantiomers of each of the pyrrolidino variants explored.

**Monday 7:00 PM**  
**Poster #26 in Exhibit Hall**  
**Is Enantiomeric Testing of Methamphetamine Necessary?**  
*Nguyen Nguyen - Soloniuk Pain Center (nguyen@soloniuk.com)*  
- In a clinical setting where controlled substances are prescribed, Urine Drug Test (UDT) results are necessary for clinical decisions. While UDT can detect recent methamphetamine use, it fails to distinguish S-methamphetamine from R-methamphetamine. At Soloniuk Pain Center (SPC) and Redding Opioid Recovery Clinic (RORC) from Northern California, enantiomeric confirmation was conducted to determine if chiral testing is necessary in these two unrelated patient populations. Of the 100 methamphetamine positive samples, S-methamphetamine represented 70% of the SPC samples and 100% of the RORC samples. With a 30% R-methamphetamine confirmation, chiral analysis for chronic pain patients is essential for informed clinical decision-making.

**Monday 7:00 PM**  
**Poster #27 in Exhibit Hall**  
**Molecular Basis for Polycystin-2 Channel Regulation and Assembly via Its C-terminal Tail**  
*Yifei Yang - Yale University (yifei.yang@yale.edu) -- *Young Investigator Grantee*  
- The C-terminal tail of polycystin-2 (PC2 Cterm) is crucial for channel regulation. Mutations in PC2 Cterm can cause autosomal dominant polycystic kidney disease. PC2 forms a calcium-permeable channel in the membrane and its function is regulated by cytosolic calcium-levels. To gain insight into how calcium-binding regulates the channel via its C-terminal tail, we characterized the conformational and dynamic responses of calcium within the PC2 Cterm, using hydrogen-deuterium exchange mass spectrometry. Our study, for the first time, provides a complete map of dynamic responses to calcium-binding within the full length C-terminal tail. Our results suggest mechanisms for functional regulation of the PC2 channel and the roles of PC2 in pathophysiology of polycystic kidney disease.
Identification of the Role of FraB in F-Asn’s Metabolism in Salmonella and Development of the Method to Extract and Quantify F-Asn from Mouse Feces

Jikang Wu - Ohio State University (wu.2014@osu.edu) -- *Young Investigator Grantee*

Fructose-asparagine (F-Asn), an amadori product from food, has been found to play an essential role for Salmonella’s growth in the inflamed intestine. Determining the role of enzymes involved in F-Asn metabolism in Salmonella will facilitate the discovery of therapeutic targets. And quantification of F-Asn from mouse feces is necessary for the study of effects on Salmonella’s F-Asn metabolism in mice model. Here a Salmonella deglycase, FraB is verified to catalyze the deglycation of F-6-phosphate-Asp producing glucose 6-phosphate and aspartate. Also the method to extract F-Asn from mouse feces is developed and isotope-labelled F-Asn is used for its quantification.

Analysis of a Toxicology Panel Using High-efficiency Cortecs Phenyl Columns

Arnie Aistars - Waters Corporation (arnie_aistars@waters.com)

High-performance liquid chromatography-tandem mass spectrometry (LC/MS/MS) has become a powerful tool for quantitative analysis of drugs of abuse in the field of forensic toxicology. While many reversed-phase columns have been used for these applications, columns that contain a phenyl functionality have shown to have unique selectivity for many drugs of abuse due to pi-pi bond interactions between the aromatic rings contained within the target analytes and the stationary phase. This poster highlights a novel, high efficiency 1.6 µm solid-core column for the separation of opioids, benzodiazepines, amines and PCP.

Rapid Evaporative Ionization Mass Spectrometry During Brain Surgery: Our Experience of Real-Time Intraoperative Tumour Characterisation

Babar Vaqas - Imperial College, London (bvaqas@gmail.com)

Rapid intraoperative identification of brain tumor tissue has the potential to improve the extent of resection of brain tumors and reduce damage to normal tissue thus improving survival and making surgery safer. A single centre study was designed utilizing Rapid Evaporative Ionisation Mass Spectrometry with 3D Ultrasound Neuronavigation to help accurately characterize brain tissue. Precise intraoperative readings from different tumor zones were taken and compared to matched core biopsy samples verified by routine histopathology. This has revealed unique in-vivo spectra for different intrinsic brain tumors and normal brain tissue. Intra-tumoral variations may shed important light into intrinsic brain tumor biology.

Sensitive and Specific LC-MS/MS Analysis of Methylmalonic Acid in Serum, Plasma and Urine

Irene Doering - RECIPE Chemicals + Instruments GmbH (doering@recipe.de)

RECIPE’s CE IVD certified ClinMass® LC-MS/MS Complete Kit, advanced – Methylmalonic Acid in Serum/Plasma/Urine (MS5100) allows the sensitive and highly selective quantitation of methylmalonic acid (MMA) in serum, plasma and urine. In samples of healthy patients the concentration of MMA - compared to succinic acid (SA) - is present in low concentrations and often requires off-line extraction or derivatisation before analysis. With our approach, the structural isomer SA is chromatographically baseline seperated and simple protein precipitation is sufficient for sample preparation. Therefore, RECIPE’s MS5100 Complete Kit allows the fast and reliable analysis of MMA and can be easily implemented in clinical routine analysis for methylmalonic acidemias.
An Investigation into Removing the Excipients from Select Oral Fluids Collection Devices by SPE and LC/MS Detection

Seyed Sadjadi - Phenomenex, Inc. (SeyedS@phenomenex.com)

Oral fluids present a convenient sample to collect and generally a non-invasive method of sample collection. Furthermore, OF is becoming increasingly popular in clinical and forensic laboratories. To address the demand, there are also increasing number of sample collection devices and some are offered with a preservative solution. These solutions may contain varying degree of excipients to maintain constant pH, stabilize the analytes and/or prevent bacterial growth in the samples. The nature and concentration of these excipients may pose difficulties with LC/MS detection of the analytes. We investigated multi-mode SPE media to substantially reduce or eliminate the preservative solution excipients.

Moving Towards the Standardization of Protein Quantification Workflows and Improving their Analytical Reproducibility

Mary Lame - Waters Corporation (mary_lame@waters.com)

High variability in protein quantification analytical data and a general lack of expertise strongly support the requirement for a standardized, kit-based approach. In this work, commercially available kits were used to quantify monoclonal antibody-based drugs in human and rat plasma. Single digit accuracy, precision, and repeatability data was achieved in experiments performed by different analysts, on different days, and with 5 unique lots of kits. Quantification limits from 10 to 500 ng/mL were achieved for all antibodies tested. Linearity of calibrators was always greater than 0.99 while accuracy and precision of quality control samples was better than 5%.

The Analysis of Common Antiepileptic Drugs in Human Urine by LC-MS/MS

Susan Steinike - Restek Corporation (Susan.Steinike@restek.com)

The use of liquid chromatography coupled with mass spectrometry (LC-MS/MS) in therapeutic drug monitoring and toxicology labs has increased significantly over the years. LC-MS provides sensitivity, speed, and the ability to simplify sample preparation. The Raptor™ Biphenyl column was developed to complement high-throughput LC-MS/MS analyses by combining the increased efficiency of superficially porous particles (SPP) with the resolution of Ultra Selective Liquid Chromatography™ (USLC™) technology. In this example, a simple dilute and shoot method was developed for 14 common antiepileptic drugs in urine using a Raptor™ Biphenyl column.

Thyroid Hormone Analysis in NIST Standard Reference Materials

Brittany Kassim - National Institute of Standards and Technology (brittany.catron@nist.gov)

The aim of this work was to develop higher order analytical methods and apply these to value assign target iodine status biomarkers, namely thyroid hormones, in applicable reference materials for the delivery of traceability and calibration tools. Method development for the quantification of thyroid hormones specifically T4 and T3 has been accomplished by way of selective elemental detection utilizing liquid chromatography (LC) coupled to an inductively coupled plasma mass spectrometer (ICP-MS). This higher order analytical method was applied to value assign target T3 and T4 hormones in currently available SRMs.

Development and Validation of a Quantitative Method for Doxorubicin/Doxorubicinol in Serum and Saliva: Special Considerations for Working with Unstable Analytes

Autumn Breaud - The Johns Hopkins University (abreaud1@jhmi.edu)

We describe the development and validation of a method for quantification of doxorubicin and doxorubicinol in human serum and oral fluid. During development of the method, we performed stability studies for this compound in various primary solutions and matrices, based upon previous studies that indicate degradation under varying conditions.
Quantitation of Serum Indoxyl Sulfate and P-Cresyl Sulfate in Chronic Kidney Disease by UPLC-MS/MS Method

Chia-Ni Lin - Chang Gung Memorial Hospital (chianilin@cgmh.org.tw)

- Chronic kidney disease causes tremendous impact because it increased risk of cardiovascular disease and mortality. Loss of kidney function induces accumulation of potentially toxic compounds, resulting in uremic retention. Indoxyl sulfate and p-cresyl sulfate are important protein-bound uremic solutes which can stimulate the progression of chronic kidney disease. A sensitive ultra-performance liquid chromatography-tandem mass spectrometry method for quantitation of indoxyl sulfate and p-cresyl sulfate in serum has been developed and can be used to follow-up the progression of disease in chronic kidney disease patients.

Quantitative Analysis of Human Tear Fluid by MALDI-TOF Mass Spectrometry

Ryan Walsh - University of Colorado, Denver (AMC) (ryan.walsh@ucdenver.edu) -- *Young Investigator Grantee*

- Identifying biochemical markers for disease is a difficult endeavor. It requires methods that can quantify multiple components simultaneously, are high throughput, cost effective and deliver high precision and accuracy. We and others are exploring the potential of matrix-assisted laser desorption/ionization (MALDI) for these applications. The approach developed in this study is a non-targeted MALDI based method to analyze human tear fluid. Our results demonstrate that precise measurements are achievable (CV values 10% or less) despite the challenges of internal standard selection, sample handling, and ion suppression. This method gives us the ability to detect, identify, and quantify biomarkers that relate to eye injury and disease. The results of this study will further reinforce the effectiveness of tear as a diagnostic tool and the potential of MALDI-TOF MS for clinical applications.

Detection of Lyme Disease Infection Through Quantification of Borrelia burgdorferi Membrane Proteins

Karen Phinney - National Institute of Standards and Technology (karen.phinney@nist.gov)

- Lyme disease is a tick-borne illness that is caused by the bacteria Borrelia burgdorferi. Diagnosis of Lyme disease in its early stages is problematic, and it generally takes several weeks before Borrelia-specific antibodies can be detected. Untreated individuals with Lyme disease can develop serious complications. We investigated the detection and quantification of B. burgdorferi membrane proteins in human serum by MRM mass spectrometry as an alternative approach to detection of bacterial infection. The bacterial protein ospA was detected at concentrations of approximately 4 fmol ospA/mg serum protein in Lyme disease patient samples; B. burgdorferi proteins were not detected in the control patient samples.

Development and Validation of a LC-MS/MS Method for the Quantification of the Checkpoint Kinase 1 Inhibitor (CHK1) CCT245737 in Human Plasma

Monique Zangarini - Newcastle University (monique.zangarini@newcastle.ac.uk)

- A LC-MS/MS method was developed and validated to quantify CCT245737, a small molecule orally active CHK1 inhibitor, in human plasma. The method requires 20µL of plasma and involve acetonitrile deproteinisation after addition of the labelled CCT245737 (IS). Detection was obtained by SRM, following the transitions m/z 379.8→360.2 for CCT245737 and m/z 384.0→324.2 for the IS. It is sensitive, precise and accurate with overall precision ≤8.5%, accuracy in the range 96%–102% and high recovery ≥93.4%. The LLOQ is 20ng/ml. The assay was validated in the range 20-20000 ng/ml. This is the first method validated to measure CCT245737 in human plasma.
Monday 7:00 PM  
Poster #43 in Exhibit Hall  
**Investigating the Lipidomic Profile Derived Through Rapid Evaporative Ionisation Mass Spectrometry of Breast Tissue Samples**  
*Merja Rossi - Imperial College London* (m.rossi@imperial.ac.uk) - *Young Investigator Grantee*  
- Rapid Evaporative Ionisation Mass Spectrometry (REIMS) is a technique used to analyse ions produced in electrosurgical smoke. This technique has recently been developed for near real time identification of normal and cancerous tissue in the form of the iKnife technology. The technology uses multivariate statistics for computational analysis of the whole lipid profile detected in the spectra derived from tissue. Here we describe how REIMS lipid profiles obtained from ex vivo breast specimens can be matched to other datasets to provide information on differences in lipid composition of breast tissue when compared with data obtained through DESI-imaging of the same clinical samples with confirmed histology.

Monday 7:00 PM  
Poster #44 in Exhibit Hall  
**Tip-based Fractionation for Comprehensive Phosphoproteome Analysis**  
*Alireza Dehghani - University of Bonn* (alirezadehghani86@gmail.com) - *Young Investigator Grantee*  
- We developed a new workflow for phosphoproteomics studies which is able to find a considerable number of phosphosites with reduced time, cost and effort. The workflow is a combination of Titanium dioxide (TiO2) phosphopeptide enrichment followed by pipette tip-based Strong Cation-Exchange (SCX) fractionation. Using this method more than 9000 phosphosites and 7500 phosphopeptides were detected out of 3 mg of HeLa lysate. The new workflow was successfully applied for the first time for the analysis of the effects of inhibition of cholesterol egress from lysosomes using U18666A inhibitor on the phosphoproteome of Mouse Embryonic Fibroblasts cells (Mef cells). 12881 phosphosites were found in this experiment which 751 were significantly regulated (349 phosphosites were up-regulated and 402 down-regulated).

Monday 7:00 PM  
Poster #45 in Exhibit Hall  
**Development of a Routine Hemoglobin Profiling Workflow**  
*Scott Peterman - Thermo Fisher Scientific* (scott.peterman@thermofisher.com)  
- Routine hemoglobin profiling is used to determine putative disease states based on glycation and/or sequence variation. Thus, analytical workflows must be sensitive to detect low-level variants and selective to characterize compounds as truncated chains, modified, altered sequence, or any combination. To achieve this, we have developed a workflow incorporating sample preparation routines using cation exchange resins to rapidly and robustly concentrate, remove matrix interference, and facilitate molecular weights cutoff extraction centered at hemoglobin chains. To test this workflow, we have evaluated neat whole blood (WB) as well as WB spiked with bovine hemoglobin at various levels.

Monday 7:00 PM  
Poster #46 in Exhibit Hall  
**Effects of Nutrient Stress on Arginine and Dimethylarginine in Primary Hepatocytes**  
*Shu-Chu Shiesh - National Cheng Kung University* (hsieh@mail.ncku.edu.tw)  
- Neonatal intrahepatic cholestasis caused by citrin deficiency, is characterized by galactosemia, hyperlipidemia, hyperammonemia, and multiple aminoacidemia. Galactose-free formulas are effective for resolving clinical symptoms. This study aimed to investigate the impacts of substitution of 18 mM glucose in culture medium by 9 mM glucose/galactose, 13.5 mM glucose or 9 mM glucose on cellular arginine, dimethylarginine and oxidative stress in primary hepatocyte. The measurement of arginine and metabolites was performed using API 5000 tandem mass spectrometer with positive ionization mode. Oxidative stress increased in hepatocytes cultured in glucose-insufficient medium, compared to 18 mM glucose medium. Intracellular concentrations of arginine and lysine did not change, but citrulline, ADMA, and SDMA increased in AML12 cultured with glucose insufficient medium.
Method Validation for Quantitation of Testosterone Calibrators: A Modification of Reference Measurement Procedures

**Ravi Orugunty - Cerilliant** (ravi_orugunty@cerilliant.com)

Development of accuracy based calibrators in biological matrices for clinical diagnostic applications requires reference measurement procedures with high accuracy and sensitivity. Testosterone presents a unique challenge with regards to the wide range of endogenous levels across female, male and age based patient populations. We wish to present our efforts towards validating a method for quantitation of Testosterone in calibrators from 0.020 ng/mL to 20 ng/mL in serum by modifying a valid reference measurement procedure. The 1000 fold range of these calibrators in serum presents unique challenges towards designing a method that will accurately measure Testosterone. Data presented will address various elements of the method validation such as precision and accuracy, linearity, limit of quantitation, recovery, matrix effects, extract stability, traceability.

A Novel [15N] Glutamine Flux Using LC-MS/MS-SRM for Determination of Nucleosides and Nucleobases

**Feng Jin - Baylor College of Medicine** (fjin@bcm.edu) -- *Young Investigator Grantee*

A novel liquid chromatography mass spectrometry (LC-MS) method is developed to quantify glutamine-derived [15N] nitrogen flux into nucleosides and nucleobases. This method will be a valuable tool to identify the nitrogen flux derived from glutamine and it can be further adaptable for high throughput analysis of large set of DNA in a clinical setting.

Patients with Celiac Disease Display a Varying Oligoclonal Antibody Response to Tissue Transglutaminase: Characterization Utilizing a Proteomic Approach

**Kari Gurtner - Mayo Clinic** (gurtner.kari@mayo.edu)

Celiac Disease (CD) is characterized by an intolerance to dietary gluten. Patients with CD often have high levels of IgA autoantibody against tissue transglutaminase (tTG). To characterize tTG reactive IgA, the autoantibodies were isolated and then analyzed by TOF-LC/MS and LC-MS/MS, using top-down and bottom-up proteomic approaches. This provided information from the variable regions of both IgA light and heavy chains to characterize tTG reactive antibodies. Comparison of positive and negative sample groups demonstrated significant light chain profile differences, indicating that celiac patients exhibit an oligoclonal response to tTG.

Development of a Quantitative MS-based Assay for Intact BNP and Its Proteolytic Variants: Early Impressions with LC and CE from “High Flow” to “No-flow”

**Koen Raedschelders - Cedars Sinai Medical Center** (koen.raedschelders@cshs.org) -- *Young Investigator Grantee*

B-type Natriuretic Peptide is a biologically active circulating factor whose concentration is routinely used in the diagnosis of heart failure. Although this analysis is routinely performed using ELISA platforms, these assays are incapable of differentiating between proteolytic forms of BNP. High-resolution mass spectrometry can easily resolve proteolytic variants with accurate quantitation, provided it is supplied with sufficiently resolved peaks. We are working on several different separation techniques that 1. Are compatible with mass spectrometry; 2. Can resolve intact BNP variants derived from a plasma matrix; 3. Can accommodate the large dynamic range with sufficient sensitivity.
**Monday 7:00 PM**  
**Poster #51 in Exhibit Hall**  
**The Application of DPX WAX Tips in Clinical Toxicology for Protein Precipitation**  
*William Kemnitzer - DPX Labs (bill.kemnitzer@dpxlabs.com)*  
- A novel method for the protein precipitation of serum was investigated using WAX dispersive pipette extraction (DPX) tips and analyzed by LC-MS-MS. Significantly, protein precipitation was performed within the DPX WAX tip to remove matrix interferences in less than 2 minutes. Viability was determined by testing the method on a comprehensive panel and comparing the results to standard protein precipitation preparations. Comparison between the two methods revealed that highly lipophilic compounds (LogP > 4) can be predicted to achieve a superior sample cleanup using the DPX WAX tips.

**Monday 7:00 PM**  
**Poster #52 in Exhibit Hall**  
**Method Validation for Nicotine and Its Metabolites by LC-MSMS Reveals a Low Clinical Utility for the Tobacco Alkaloid Anabasine**  
*Matthew Feldhammer - Emory University (matthew.feldhammer@emory.edu) -- *Young Investigator Grantee*  
- The need to provide accurate and quantifiable data in the detection of patient adherence to smoking cessation programs necessitates the utilization of high-resolution instrumentation. Reliance on immunoassay-based approaches can lack the sensitivity and specificity to provide a complete clinical picture in the context of various nicotine replacements and smoke cessation therapies. In the healthcare setting, the ability to provide clinicians with this information can have a significant impact on organ allocation and transplantability in addition to informing surgical eligibility. Anabasine, an alkaloid present in tobacco plants, is often utilized as a primary marker of active smoking. Surprisingly, during our validation of a new LC-MSMS assay, we determined that this utilization resulted in a very high false negative rate when compared to patients’ self-reported smoking status.

**Monday 7:00 PM**  
**Poster #53 in Exhibit Hall**  
**Separating Vitamin D2 D3, their 25-OH Metabolites and C-3 Epimers**  
*Ken Tseng - Nacalai USA Inc. (ken@nacalaiusa.com)*  
- The accuracy of current vitamin D measurements by immunoassays and LCMS has been questioned due to the overlapping LC peaks with identical m/z values epimers and isobars. To solve this problem, we have developed a new HPLC method to achieve baseline separation of vitamin D2/D3, their 25-OH metabolites and C3-epimers in one single run.

**Monday 7:00 PM**  
**Poster #54 in Exhibit Hall**  
**Detecting THC Metabolites and Other Cannabinoids**  
*Toshi Ono - Nacalai USA Inc. (ono@nacalaiusa.com)*  
- In the first part, Δ9-THC, 11-hydroxy-Δ9-THC and 11-nor-9-carboxy-Δ9-THC are detected using a simple gradient. In the second part, four cannabinoids, CBD, CBN, Δ9-THC, and Δ8-THC were baseline separated making quantification easy.

**Monday 7:00 PM**  
**Poster #55 in Exhibit Hall**  
**A Sensitive Liquid Chromatography–Tandem Mass Spectrometry Method for the Simultaneous Determination of Serum Estradiol, Estrone, and Estriol**  
*Feng Bai - LABioMed at Harbor-UCLA Medical Center (fbai@labiomed.org)*  
- We developed and validated a highly sensitive LC-MS/MS method for the simultaneous measurement of serum E1, E2, and E3 for clinical and research purposes in both women and men. The three estrogens were separated on a selected column within 3 minutes and detected on API5000 with ESI source at negative mode. The assay sensitivity reached 2 pg/mL without using sample derivatization and other sensitivity enhancing techniques. The assay precision (%CV) were 2.6 to 5.6 for E1, 4.3 to 5.2 for E2, and 4.1 to 8.7 for E3. The accuracy (%) were from 95.6 to 99.0 for E1, from 96.8 to 98.4 for E2, and from 94.7 to 97.3 for E3 respectively at spanning different estrogen concentrations.
Optimization of Derivatization Reaction Used in Sample Preparation Method in Analysis of Methylmalonic Acid in Plasma for Clinical Research

Mindy Gao - Thermo Fisher Scientific (mindy.gao@thermofisher.com)

- Methylmalonic acid (MMA) is a polar molecule that poses challenges for the development of quantitative LC-MS methods. Two analytical approaches have been implemented: analysis of MMA in negative ionization mode and analysis of derivatized MMA in positive ionization mode. The product of the derivatization reaction with n-butanol shows improved reverse phase chromatographic retention and higher ionization efficiency than underivatized MMA, making this method a preferred quantitative solution. The derivatization reaction parameters described in the literature resulted in variable, up to 100 fold, reaction efficiency. Several reaction parameters were investigated and optimized to ensure reproducible and efficient butylation reaction of MMA.

LCMS Based CSF Neurotransmitter Quantification for Following Psycho-pharmacotherapy in Psychiatric Disorders

Dimitri Brinet - Sahlgrenka Academy at Gothenburg University (dimitri.brinet@neuro.gu.se) -- *Young Investigator Grantee*

- Psychiatric disorders such as depression and bipolarity are leading causes of disability and have huge socioeconomic consequences. The molecular mechanisms underlying psychiatric diseases still remain elusive. Pharmacotherapy of these conditions aim at modulating the neurotransmitter equilibrium in the synaptic cleft. However, appropriate molecular markers to monitor psycho-pharmacotherapy effects are not available. We developed a SPE-LCMS method for quantification of neurotransmitters in CSF. Neurotransmitter quantification was employed to establish comprehensive CSF profiles in suicidal patients that underwent psychopharmacotherapy. The data aid to improve diagnosis, prognosis of psychiatric conditions as well as monitor treatment effects and provide insight in the underlying molecular pathology.

Structure Specific Immunolabeling and Mass Spectrometric Probing of Amyloid Beta Plaque Pathology in Alzheimer's Disease

Wojciech Michno - Sahlgrenka Academy at the University of Gothenburg (wojciech.michno@neuro.gu.se) -- *Young Investigator Grantee*

- Alzheimer's disease (AD) is a chronic, neurodegenerative disease, of which the underlying pathological mechanism is still not understood. The disease is characterized by accumulation of amyloid-β (Aβ) peptides into different extracellular plaques. Plaques have also been found in non-demented pathological ageing patients. Therefore, discrimination between structural and molecular plaque architecture are of essential interest to resolve Aβ plaque pathology in AD. Here, hyperspectral imaging paradigm employing the Aβ aggregate binding luminescent conjugated oligothiophenes (LCO) in combination with an in-house software was used to differentiate between different types of plaques. The approach was further shown to be applicable for laser microdissection and offline mass spectrometric analysis, which validated the presence of various C-terminal Aβ in the plaques.

Polarity Switching Mass Spectrometry Imaging of Healthy and Cancerous Hen Ovarian Tissue Sections by IR-MALDESI

Milad Nazari - North Carolina State University (mnazari@ncsu.edu) -- *Young Investigator Grantee*

- Mass spectrometry imaging (MSI) is a rapidly evolving field for monitoring the spatial distribution and abundance of analytes in biological tissue sections. It allows for direct and simultaneous analysis of hundreds of different compounds in a label-free manner. In order to obtain a comprehensive metabolite and lipid data, a polarity switching MSI method using infrared matrix assisted laser desorption electrospray ionization (IR-MALDESI) was developed and optimized where the electrospray polarity was alternated from one voxel to the next. Healthy and cancerous ovarian tissue sections were analyzed using this method. Distribution and relative abundance of different metabolites and lipids within each tissue section were discerned, and differences between the two were revealed.
Monday 7:00 PM
Poster #60 in Exhibit Hall

**Improved Speed & Reproducibility of Protein Digestion Using Novel Sample Preparation Technology**

*Sherry Gregory - Thermo Fisher Scientific (sherry.gregory@thermofisher.com)*

‣ Currently overnight in-solution trypsin digestion of proteins is used during peptide mapping; however this protocol requires a number of steps, which can differ between laboratories, making method transfer and data analysis between user groups problematic. Additionally, due to the number of steps required, in-solution digestion can increase the potential for user error. As a result, this methodology often leads to variations in the chromatographic profile and complicates the adoption of robust, generic workflows. Here we describe a workflow including novel, rapid and precise digestion of Cytochrome C, followed by micro-elution solid phase extraction (SPE) clean-up and analysis with next generation UHPLC and high resolution mass spectrometry detection (UHPLC-HRMS).

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Monday 7:00 PM
Poster #61 in Exhibit Hall

**Rapid Evaporative Ionisation Mass Spectrometry (REIMS) in Endoscopy: Preparing for Clinical Translation**

*James Alexander - Imperial College, London (j.alexander@imperial.ac.uk) -- *Young Investigator Grantee**

‣ Rapid Evaporative Ionisation Mass Spectrometry (REIMS) in endoscopy utilises the aerosol released during electrosurgical tissue dissection through integration with an endoscopic polypectomy snare. A significant barrier to its clinical usefulness is the potential delayed signal transfer and loss of signal intensity resulting from aspiration of aerosol from a closed cavity with a long sampling line. We show experiments comparing a novel direct method for introduction of aerosol to the mass spectrometer. The novel method produced a robust signal comparable to the original Venturi setup, while reducing cut-to-signal time by >50%. It has shown good results in 10 procedures on patients.

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Monday 7:00 PM
Poster #62 in Exhibit Hall

**Newborn Screening Tests for Metabolic Disorders Using Tandem Mass Spectrometry in Korea - Report from One Laboratory**

*Yoonjoo Kim - EONE Laboratories (yjkim@eonelab.co.kr)*

‣ We summarized the data of newborn screening tests in EONE Laboratories from January 2013 to September 2015, and compared the results with the previous reports in Korea. A total of 155,331 dried blood specimens (DBS) were analyzed for 11 amino acids and 14 acylcarnitines using MS/MS (API 2000, AB Sciex, Canada). 0.6% of all screened samples were positive in the initial screening test. We recommend the second screening test to confirm the positive marker for these samples. Of these, 976 repeat samples were available for retest. After the second screening test, one hundred eighty five samples were positive again; 92 positive samples for amino acids, with phenylalanine being the most common; and 93 positives for acylcarnitines, C5-acylcarnitine as the most common. Regarding positivity rate and a spectrum of abnormal analytes, the results were similar to those reported previously.

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Monday 7:00 PM
Poster #63 in Exhibit Hall

**Continuing Development of BDX003 a Serum-based MALDI-TOF Test to Detect Hepatocellular Carcinoma in High-risk Patients**

*Nicholas Dupuis - Biodesix, Inc. (nicholas.dupuis@biodesix.com)*

‣ BDX003 is a serum protein test combining MALDI-TOF with an AFP ELISA which classifies patients into two groups (HCC or NoHCC). The test was initially developed with two sample sets totaling 158 from HCC patients at various stages, and 135 patients with liver disease but no HCC. This development effort resulted in a test which detects HCC with 80% sensitivity and 79% specificity in the validation cohort. Here we present ongoing work to further characterize the BDX003 assay. HCC detection sensitivity will be tested in at least one independent sample cohort with a focus on early stage (I/II) cancer. We will also present results from pilot studies to evaluate reproducibility, stability, and cross platform portability of the test.
**Comparison of Extraction Methods for the Quantification of Eculizumab from Serum Using Microflow LC-ESI-Q-TOF Mass Spectrometry**

*Paula Ladwig* - Mayo Clinic (ladwig.paula@mayo.edu)

As monoclonal antibody therapeutics become humanized, tryptic peptide approaches for quantitation of biologics in serum become more challenging. An alternative is to monitor the unique molecular mass of the intact light chain. The ability to selectively extract only the IgG4 antibodies from serum should allow for an advantage in detection. The IgG4 extraction compared to the extraction of all IgG immunoglobulins allowed for a ~10-fold lower limit of quantitation for eculizumab. This approach could be beneficial for the therapeutic monitoring for IgG4 biologics that need a lower limit of detection and the specificity that other approaches are unable to provide.

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**Incorporating Analysis of Mitragynine into LC-ESI-MS/MS Methodology Routinely Used for Quantification of Pain Medication and Illicit Drugs in Urine**

*Katherine Yahvah* - Kashi Clinical Laboratories (kyahvah@kashilab.com)

We describe development and validation of a 6.5 minute LC-ESI-MS/MS method for quantification of mitragynine in human urine for monitoring of kratom use. Methadone-d3 is used as internal standard. A between-laboratory comparison of concentrations was performed with mitragynine concentrations across the analytical measurement demonstrating acceptable correlation. Our laboratory has routinely measured mitragynine in urine samples for > 1 year with an overall CV for QC samples of 9.3% and accuracy of 102.3%. The methodology we describe allows for measurement of mitragynine within routinely used sample analysis techniques for pain medication and illicit drugs, enabling easy implementation of mitragynine testing.

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**Ambient Mass Spectrometry Imaging for Assessing P53 Mutation Status in Breast Cancer**

*Jialing Zhang* - UT Austin (jialingzhang@utexas.edu) -- *Young Investigator Grantee*

TP53 gene mutations are the most frequent genetic alterations in cancer, occurring in 20%-30% human breast cancer. Cancer bearing TP53 mutations are prone to be aggressive and are associated with poor overall and disease-free survival in breast cancer. In this study, desorption electrospray ionization mass spectrometry imaging (DESI-MSI) was utilized to chemically map breast cancer tissues, including p53 mutations positive tumor tissues, p53 mutations negative tumor tissues, and normal breast tissues. The methodology allowed prediction of the occurrence of TP53 gene mutations directly from breast cancer tissue based on the detection of specific lipid patterns, and may become a valuable method for assessing p53 status in clinical specimens.

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**LC-MS/MS Analysis of 25 Opioids from Dried Urine Spots**

*Jessica Boyd* - Calgary Laboratory Services/University of Calgary (jessica.boyd@cls.ab.ca) -- *Young Investigator Grantee*

Dried urine spots are not commonly used in the clinical toxicology laboratory despite being a convenient and economical alternative to traditional liquid specimens. Here we describe the development of an LC-MS/MS assay for detection of 25 opioids (including pain management drugs, drugs of abuse and designer drugs) from DUS.

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**Development and Validation of LC-MS Based Autotaxin Functional Assay and Autotaxin Inhibitors Screening by PUF-LCMS**

*Yongchao Li* - University of Illinois at Chicago (yli74@uic.edu) -- *Young Investigator Grantee*

After identification of the biomarker and treatment target of asthma by LC-MS based lipidomics and we develop and validate LC-MS based Autotaxin functional assay and screen the inhibitors from mixture (botanical extracts) by PUF-LCMS.
**Quantitative Analysis of Protein Expression in Zebrafish Embryos Neuronally Expressing the Human EWSR1-ERG Oncogene**

*Dana Ohana - Leiden University Medical Centre (dohana@lumc.nl) -- *Young Investigator Grantee*

• Ewing sarcoma, a pediatric bone sarcoma, is characterized by a reciprocal translocation event between EWSR1 and a gene of the ETS family. A binary transgenic zebrafish model for Ewing's sarcoma has been recently developed, which expresses EWSR1-ERG neuronally and GFP for monitoring. A bottom-up proteomics approach was performed on embryos expressing EWSR1-ERG and on wild type embryos. Spectral counting was used to calculate the changes between the mutated and wild type fish. A variety of the up and downregulated proteins were involved in pathways, such as oncogenesis, transcription and translation and cellular respiration, which were repeatedly associated with Ewing's sarcoma.

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**Multiplexed Quantification of a Serum Protein Panel to Monitor Treatment of Duchenne Muscular Dystrophy Patients**

*Linda Switzar - Leiden University Medical Center (l.switzar@lumc.nl) -- *Young Investigator Grantee*

• Duchenne muscular dystrophy (DMD) is a genetic disorder that is characterized by continuous muscle damage. Recently, a novel drug therapy aimed at muscle restoration and delay of disease progression has been conditionally approved for treatment of patients that suffer from this severe and fatal disease. Besides the established functional outcome measures, protein biomarkers offer an attractive alternative for monitoring the effectiveness of treatment. In this study, an established combination of immunocapture and mass spectrometry (MS) will be employed for serum protein quantification in a multiplexed assay for evaluation of various DMD biomarker candidates.

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**The Role of UHPLC-MS/MS in Preclinical and Clinical Studies of Drug Interactions with Botanical Dietary Supplements**

*Richard van Breemen - University of Illinois College of Pharmacy (breemen@uic.edu)*

• Inhibition or induction of cytochrome P450 (CYP) enzymes and transporters are responsible for most drug-botanical interactions, and MS-based assays facilitate the pre-clinical and clinical assessment of these interactions. For inhibition of CYP enzymes by botanical dietary supplements, we utilize UHPLC-MS/MS with CYP substrate cocktail inhibition assays to measure activity of multiple CYP isoforms. Preclinical models of induction of CYP enzymes and transporters are carried out using human hepatocytes supported by UHPLC-MS/MS based functional CYP assays. To confirm interactions predicted in vitro, clinical trials of drug-botanical interactions are carried out based on pharmacokinetic studies of known CYP substrates supported by UHPLC-MS/MS.

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**Development of a Rapid LC-MS/MS Method for Human Serum Lipid Mediator Profiling**

*Ben Figard - Shimadzu Scientific Instruments (bfigard@shimadzu.com)*

• Lipid mediators are bioactive lipids which play a role in many biological functions, including immune dysfunction after severe inflammation. Recent development of a high sensitivity ultra-fast mass spectrometer enables lower detection limits for lipid mediator species. A comprehensive and highly sensitive application for the analysis of lipid mediators and their metabolites using a triple quadrupole mass spectrometer is presented here. Method conditions were developed to simultaneously analyze 158 lipid mediator-related compounds. A single chromatographic analysis is capable of separating a wide range of positive and negative species such as hydrophilic metabolites, tetranor-PGs and hydrophobic arachidonic acid.
Monday 7:00 PM
Poster #73 in Exhibit Hall
**Identification of Anaerobic Bacteria from BACTEC and BacT/Alert Anaerobic Blood Culture Media Using the Bruker MALDI Sepsityper Kit and MALDI-TOF MS**

*Jogarao Vedula* - Div. of Clinical Microbiology, Icahn School of Med (joe.vedula@gmail.com)

- In this study, the accuracy of identification of anaerobic microorganisms from two different anaerobic blood culture (BC) media using the Bruker MALDI Sepsityper kit followed by MALDI-TOF MS was evaluated. Comparison of the BACTEC and BacT/ALERT systems for detection of anaerobic bacteria showed that the BACTEC instrument was more rapidly able to detect anaerobic organisms spiked into the BACTEC BC bottles (median 43.13h) as compared to the BacT/ALERT BC bottles (median 65.12h). Conversely, anaerobic organisms present in the BacT/ALERT BC bottles were more accurately identified by MALDI-TOF MS after Sepsityper processing (15/26; 58%) than the BACTEC BC bottles (6/26; 23%). The MALDI Sepsityper method must be further refined for identification of anaerobes from positive blood culture bottles to enable more accurate identification of these organisms.

Monday 7:00 PM
Poster #75 in Exhibit Hall
**Point-of-care Identification of Ingested Intoxicants by Thermal Desorption Electrospray Ionization/Mass Spectrometry in the Emergency Room**

*Chi-Wei Lee* - Kaohsiung Medical University (chiweilee1964@gmail.com) -- *Young Investigator Grantee*

- To expedite rescue of intoxicated patients in the emergency department, we developed an analytical method for rapid identification of ingested intoxicants by thermal desorption-electrospray ionization mass spectrometry. Since no pretreatment of the specimen is required, the whole analytical process could be completed within 15 seconds. This technique, together with informational support provided by online mass spectral database, allows for early non-invasive point-of-care identification of ingested intoxicants in the oral fluid or gastric lavage content of intoxicated patients, and is promising in providing important toxicological information for decision-making during critical resuscitation in a timely manner, and hence ensuring the appropriateness of the succeeding management.

Monday 7:00 PM
Poster #76 in Exhibit Hall
**LDTD-MS/MS Method for Quantitative Analysis of Four Immunosuppressant Drugs in Whole Blood and Cost Analysis Comparison to LC-MS/MS**

*Stephen Merrigan* - ARUP Institute for Clinical and Experimental Path (stephen.d.merrigan@aruplab.com)

- Accuracy, turnaround time, and analytical cost are important factors to consider when developing a therapeutic drug monitoring assay for immunosuppressive drug therapy. Sirolimus, Cyclosporin A, Tacrolimus, and Everolimus therapies are monitored to balance therapeutic efficacy and prevent organ rejection, while minimizing the adverse effects associated with high concentrations in whole blood. Laser Diode Thermal Desorption Tandem Mass Spectrometry (LDTD-MS/MS) technology can provide rapid results and reduced analytical costs associated with mobile phases and liquid chromatography columns. An eight second LDTD-MS/MS method was developed for the quantification of four immunosuppressive drugs, in whole blood. Method validation data and cost analysis are presented.

Monday 7:00 PM
Poster #77 in Exhibit Hall
**Ionization Response of Stable Isotope Labeled Small Molecules and the Potential Impact on LC/MS/MS Assays**

*Sarah Aijaz* - Cerilliant Corporation (sarah_aijaz@cerilliant.com)

- LC/MS/MS assays of stable isotope labeled compounds and their native counterparts were compared to investigate relative ionization responses. Native, deuterated, and 13C analogs of Testosterone, Pregabalin, and L-Thyroxine were chosen as representative small molecules. Ionization responses were not equivalent between native and labeled compounds analyzed under identical conditions and concentrations. The magnitude of ionization response differences is affected by experimental parameters such as collision energy. Assays performed at multiple collision energies demonstrated the relative ionization responses can be varied by greater than 20%. These ionization response differences must be evaluated, understood, and optimized when considering the use of stable labeled standards for quantitation.
Monday 7:00 PM
Poster #78 in Exhibit Hall
**Determination of Urinary Opioids by Solid-Phase Extraction LC-MS/MS for Clinical Research: Comparison of Automated and Manual Sample Preparation**
*Teresa Pekol - Extend Consulting (tpekol@hotmail.com)*

- Automated sample preparation improves laboratory operations by a) reducing errors in sample tracking and preparation, b) producing more consistent results free of analyst-to-analyst variation, c) allowing analysts to work more efficiently, and d) minimizing laboratory hazards in regard to solvent exposure and repetitive motions associated with manual pipetting. For labs considering automated sample preparation, the aim of this study was to compare the performance and benefits of a Tecan Freedom EVO® 100 liquid handler to manual sample preparation using a routine clinical research application.

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Monday 7:00 PM
Poster #79 in Exhibit Hall
**Amphetamine- and Methamphetamine-like Compounds Identified in Urine from an Over-The-Counter Dietary Supplement**
*Justin Wotring - InSource Diagnostics (justinw@insourcedx.com)*

- Two compounds were identified in urine specimens from a pain management clinic that resembled both Amphetamine and Methamphetamine. Upon speaking with the physician, it was noted that the patient denied illicit Methamphetamine use, but admitted to taking an over-the-counter dietary supplement known as “Meltdown”. Two of the compounds listed in the ingredients were R-Beta-Methylphenylethylamine and Synephrine HCl. This work shows the similarities between the ingredients in the dietary supplement with Amphetamine and Methamphetamine that were discovered through a SPE LC-MS/MS procedure, and how accurate identification is achieved.

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Monday 7:00 PM
Poster #80 in Exhibit Hall
**Translational Bioinformatics for Mass Spectrometry Imaging in a Clinical Research Setting**
*Bindesh Shrestha - Waters Corporation (Bindesh_Shrestha@Waters.com)*

- Mass Spectrometry Imaging (MSI) is an emerging technology in pathology research that generates hundreds of gigabytes of detailed molecular data of potential importance. Effective translation of MSI data into biologically or clinically useful information requires advanced computational solutions. Here, an integrated bioinformatics research platform is presented that allows intuitive histology-directed interrogation of MSI datasets for tissue-specific biomarker recovery, automated tissue classification and entropy driven tumour heterogeneity assessment.

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Monday 7:00 PM
Poster #81 in Exhibit Hall
**Quantification of Glycosaminoglycans (CS, DS and HS) in Dried Urine Spots by UPLC-MS/MS**
*David Millington - Duke University Hospital (dmilli@duke.edu)*

- Dried urine spots (DUS) on filter paper are readily shippable in the mail to a distant laboratory for analysis. We have adapted a previously developed UPLC-MSMS method of analyzing the glycosaminoglycans (GAGs) CS, DS and HS, in liquid urine to extracts of DUS for this purpose. A fixed amount of d3-creatinine is added to a 2 cm diameter disk excised from a DUS, and creatinine and GAGs are co-extracted. An aliquot of the extract is analyzed for creatinine and the remainder is dried, then methanolysed to produce dimeric subunits derived from the principal GAGs. A mixture of isotope-labeled dimers, prepared from standard GAGs by deuteriomethanolysis, enables quantification by pseudo-isotope-dilution. This assay has sufficient sensitivity, precision and accuracy to reliably measure elevated urinary GAGs in DUS from patients with known or suspected mucopolysaccharidoses.
**Monday 7:00 PM**  
**Poster #82 in Exhibit Hall**  
**A UHPLC-MS/MS Method for Asymmetric Dimethyl Arginine (ADMA) a Prognostic Biomarker Among Patients with End-Stage Renal Disease**  
*Amber Gray - Mayo Clinic Foundation (gray.amber@mayo.edu)*

- ADMA has been previously implicated in all-cause mortality in patients with ESRD and is useful as a biomarker to predict adverse outcomes in a high risk population. Current methods for measuring ADMA concentrations are not optimized for clinical workflows as they often involve cumbersome sample preparation or lengthy liquid chromatography to separate the symmetric dimethyl arginine (SDMA) isomer. We developed a facile, rapid and reproducible UPLC-MS/MS method for ADMA that is ideal for implementation in a clinical lab. Detection of ADMA and the C13-ADMA internal standard was achieved in ESI mode using an API 3200 (AB Sciex) coupled with a Dionex Ultimate 3000 RS UHPLC system (ThermoScientific). Total analysis time was 7.17 minutes per sample with only 2 minutes sent to the mass spectrometer allowing for multiplexing of the assay to further reduce analysis time.

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**Monday 7:00 PM**  
**Poster #83 in Exhibit Hall**  
**Metanephrines in Urine by Liquid Chromatography Tandem Mass Spectrometry**  
*Magdalena Rajska - Spadia Lab (magdalena.rajska@spadia.cz)*

- Neuroendocrine tumors, such as pheochromocytomas or paragangliomas, represent a clinically and etiologically diverse group of disorders. These tumors exhibit increased production of catecholamines and their metabolites and therefore quantification of biogenic amines is used for their differential diagnosis. The aim of this work was to develop the LC-MS/MS method based on hydrophilic interaction liquid chromatography which provides possibility for quantification of wider group of analytes related with neuroendocrine tumors. Method for quantification of metanephrines in urine fulfilled validation requirements.

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**Monday 7:00 PM**  
**Poster #84 in Exhibit Hall**  
**Categorizing and Differentiating of Clinically Isolated Mycobacteria by Differential Pattern Analysis of MALDI-TOF MS Data**  
*Kyu Park - ASTA, Inc. (kyuhpark@maldiplate.com)*

- The use of MALDI-TOF MS has become a powerful and popular method to identify various pathogenic bacteria in many clinical laboratories. However, mycobacterium species are still challenging to correctly identify by MALDI-TOF MS. Fifty mycobacterial isolates obtained from patients were selected to include 20 species, identified by PCR analysis, and analyzed by a MALDI-TOF mass spectrometer to investigate the effect of culture condition, sample preparation, and MALDI peak selection. Phylogenetic trees based on MALDI spectrum were used to show the differentiation and the categorization of the isolates.

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**Monday 7:00 PM**  
**Poster #85 in Exhibit Hall**  
**Antibody-Independent SRM Strategies for Ultrasensitive and Multiplexed Quantification of Cancer Biomarker Candidates**  
*Tujin Shi - Biological Sciences Division (tujin.shi@pnnl.gov) -- *Young Investigator Grantee*

- Selected reaction monitoring (SRM)-based targeted quantification provides good selectivity, reproducibility, sensitivity, and multiplexing capability rendering it highly suitable for robust, high-throughput and cost-effective verification of cancer biomarker candidates. The ability of SRM-MS to detect and quantify low abundance proteins present in blood plasma/serum at low ng/mL or even lower levels, however, relies on the front-end enrichment through specific affinity reagents (e.g., antibodies). To address this limitation, we have recently developed two antibody-independent, targeted quantification capabilities (i.e., PRISM-SRM and LG-SRM) that enable protein quantification at low or sub ng/mL levels in plasma/serum. Relevant applications for protein biomarker quantification will be presented.
**Extraction of Urinary Hormone Metabolites from Urine Using Supported Liquid Extraction Prior to HPLC-MS/MS Analysis**

**Kristin Jones - Biotage** (kristin.jones@biotage.com)

- Estrogen, androgen, and glucocorticoid metabolism can be used to assess overall hormonal balance during hormone therapy. Urine is the recommended testing matrix for quantification of primary estrogen levels as well as secondary estrogen metabolites when monitoring overall hormone balance, therapy, and detoxification; non-invasive collection allows for sampling over a 24-hour period, providing insight to circadian rhythm. Since many samples are generated for a single patient in one day, a fast and robust testing protocol is needed during clinical testing. Here we demonstrate a rapid and reliable sample preparation method using SLE+ to extract a suite of 30 hormone analytes from a hydrolyzed urine matrix. LC-MS/MS analysis in a single injection shows that matrix effects are eliminated by the SLE+ protocol and that analyte recovery and sensitivity are adequate for clinical interpretation.

**Direct Injection of Serum and Online Solid Phase Extraction for the Quantification of 35 Benzodiazepines and Metabolites by Liquid Chromatography MS/MS**

**Valérie Thibert - Thermo Fisher Scientific France** (valerie.thibert@thermofisher.com)

- An analytical method for the quantification of 35 benzodiazepines and metabolites that allows for direct injection of human serum is reported. Conventional HPLC methods require manual offline sample preparation; in this case, internal standards are automatically added to each sample by the autosampler prior to injection of the intact serum onto an online SPE liquid chromatographer using a Thermo Scientific™ Transcend™ II system. Analytes are detected by mass spectrometry in single reaction monitoring acquisition mode on a Thermo Scientific™ TSQ Endura™ triple quadrupole with a heated electrospray ionization source. The method was analytically validated in terms of limits of quantification, linearity ranges, accuracy and precision for each analytes using the MS9050 ClinMass® TDM Platform from RECIPE with the MS9550 Add-On Set for Benzodiazepines.

**Automated Desorption, SPE Extraction, and LC/MS/MS Analysis of Dried Blood Spots**

**Matthew Arnold - Gerstel, Inc.** (mjarnold@gerstelus.com)

- In this report, the complete automation of dried blood spot (DBS) analysis is demonstrated. DBS cards are inserted automatically into a flow through cell in which individual blood spots are rapidly and effectively desorbed. The DBS elution is integrated into a complete cleanup and analysis system using online SPE with replaceable cartridges combined with automated injection to an LC/MS/MS system. Automated DBS extraction methods were optimized for a variety of analytes from rat and bovine blood. The resulting precision and accuracy data are provided.

**Metabolomic Profile Change in Type 2 Diabetes Revealed by Commercial Metabolomics Kit with Mass Spectrometry**

**Sang-Guk Lee - Yonsei University College of Medicine** (comforter6@yuhs.ac)

- We measured 188 metabolites including acylcarnitines, amino acids, biogenic amines, glycerophospho- and sphingolipids, and hexose with the AbsoluteIDQ p180 kit from Biocrates Life Science using Agilent HPLC 1260 and AB Sciex 5500 QTrap in five patients with T2DM and five healthy controls. Each 188 metabolites were compared by Mann-Whitney test. We found eighteen statistically different metabolites, six metabolites increased and twelve metabolites decreased in patients with T2DM. In addition, the patients with T2DM and healthy controls were separated with little over-lap using principal component analysis. Especially branched chain amino acid, leucine, isoleucine and valine were increased in patients with T2DM.
Monday 7:00 PM  
Poster #91 in Exhibit Hall  
**Challenges of ICP-MS Method Development for Routine Clinical Analysis**  
*Joshua Akin - UC San Diego Health System (jakin@ucsd.edu)*  
- We developed a quantitative method for analysis of As, Cd, Hg and Pb in clinical whole blood samples using ICP-MS.  
We evaluated previously published strategies for ICP-MS internal standard selection, acid wash concentration and matrix-matching calibrators. Internal standardization can help correct for non-spectral interferences. Rhodium and Iridium performed optimally for all four analytes. Wash cycle duration proved more effective than acid rinse concentration for reducing Mercury memory effects and preventing carryover. We showed that four commonly used whole blood anticoagulants can be suitable for matrix-matching calibrators. Development of analytical methods for ICP-MS can be challenging and several factors must be considered in the validation phase.

Monday 7:00 PM  
Poster #92 in Exhibit Hall  
**Detection of UCN3 as a Biomarker for Obstructive Sleep Apnea in Children Using Multiple Reaction Monitoring**  
*Tyler Yin - University of Louisville (d0yin001@louisville.edu) -- *Young Investigator Grantee*  
- Obstructive sleep apnea (OSA) is a disorder where a person is deprived of oxygen that may cause additional health problems if left untreated. Children with OSA are thought to be underdiagnosed due to the lack of sleep centers around the country and noncompliance with take-home testing. Urocortin-3, (UCN3) has been previously identified as a urine biomarker for OSA in children. Here, we utilized multiple reaction monitoring to identify a peptide fragment that gave 3 transitions with high signal intensity. We find that the linearity and sensitivity are sufficient to make a differentiation between children with and without OSA based on previous findings. We also developed two methods in parallel that deplete abundant proteins and concentrate UCN3 in both urine and plasma spiked samples. Both methods yield highly purified UCN3 that are scalable for high throughput assays.
Tuesday 5:00 PM
Poster #1 in Exhibit Hall
**Determination of Monosialogangliosides in Human Plasma by a Novel UPLC/MS/MS Assay in Combination with Chemical Derivatization**
*Qianyang Huang* - *Cleveland State University* (qyhuang0330@gmail.com)

In this study, a novel reverse phase UPLC/MS/MS method for determination of three monosialoganglioside species, GM1, GM2, and GM3, in human plasma has been developed and validated. This assay employed DMTMM & PAEA chemical derivatization for signal enhancement and D3-labeled monosialogangliosides as internal standards (IS). The analytes and ISs were extracted from plasma using protein precipitation procedure, cleaned up with liquid-liquid extraction, and derivatized with DMTMM & PAEA. Thereafter, the samples were injected into a Shimadzu Nexera UHPLC system interfaced to an AB Scix Qtrap 5500 mass spectrometer that operating in ESI positive and Multiple Reaction Monitoring (MRM) mode to achieve highly sensitive and specific detection.

Tuesday 3:00 PM
Poster #2 in Exhibit Hall
**Discovering Diabetic Lipid Biomarker Using HRAM LC-MS-MS Approach on a High Field Hybrid Quadrupole-Orbitrap Mass Spectrometer**
*Reiko Kiyonami* - *Thermo Fisher Scientific* (reiko.kiyonami@thermofisher.com)

Lipids play a key role in cell, tissue and organ physiology with diseases such as diabetes which involve disruption of their metabolic enzymes and pathways. Identification of unique lipid biomarkers to distinguish healthy humans compared to those with a disease can have an impact on the early detection of diseases and personalized medicine. Here we demonstrate that HRAM LC MSn approach on a high filed hybrid quadrupole Orbitrap mass spectrometer enables rapid putative biomarker discovery through lipidomics profiling experiments. Two phenotypes of the rat (ZDF vs. lean wild type) plasma samples were used as a model case.

Tuesday 5:00 PM
Poster #3 in Exhibit Hall
**DESI-imaging: Histology Applications**
*Renata Soares* - *Imperial College, London* (r.filipe-soares@imperial.ac.uk)

Desorption Electrospray Ionization (DESI) has been utilized across several subjects ever since its development in 2004. One major potential application of this break-through technique is as a diagnostic tool for cancer. By looking at biochemical composition of tissues, DESI-MSI is able to differentiate between types of tissue, cancers and cancer stages hence providing a simpler, faster, user independently diagnosis having major implications in cancer management and costs.

Tuesday 3:00 PM
Poster #4 in Exhibit Hall
**A Novel Automated Sample Prep Process for an Improved LC/MS/MS 25-hydroxy Vitamin D Method**
*Joyce Flanagan* - *Marshfield Clinic* (flanagan.joyce@marshfieldclinic.org)

Our aim was to develop and validate an automated front-end extraction process for vitamin D including an improved LC/MS/MS method. Complete automation was achieved with the Tecan AC extraction plate on a Tecan EVO 100 system, whereas 25-OH Vit D3 and 3-epi-25-OH Vit D3 were chromatographically separated with a Phenomenex, Kinetex, 2.6 µm, pentfluorophenyl (FS) column on a Waters Acquity UPLC Xevo TQ-S LC/MS/MS system. We demonstrated improved assay efficiency, accuracy, and turn-around-time by reducing the sample prep time from a 2.5 hour manual extraction to a 45 min hands-free process and analytical time from 8 to 4 minutes per sample.
**Tuesday 3:00 PM**
**Poster #6 in Exhibit Hall**

**Simple and Cost-effective Generation of LC-MS/MS Interference Testing Materials**

*Richard King - PharmaCadence Analytical Services* (rick.king@pharmacadence.com)

- Interference testing is a critical component of the method validation process for a routine clinical laboratory test. One source of potential interferences in LC-MS/MS are the phase II metabolites of the analyte. While it is possible to purchase some of the more common glucuronide metabolites for testing, they are expensive and not all are stable. By using human liver microsomes fortified with the appropriate co-factors, the glucuronide conjugates can be produced in sufficient quantities to perform interference testing at a relatively low cost. Results will be shown for steroid hormones Androstenedione, Desoxycortisol, Cortisol, DHEA, Deoxycorticosterone, 17-Hydroxypregnenolone, Progesterone, 17-Hydroxyprogesterone, and Testosterone.

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**Tuesday 5:00 PM**
**Poster #7 in Exhibit Hall**

**Liquid Chromatography Mass Spectrometry Applications in a Newborn Screening for Mucopolysaccharidoses**

*Francyne Kubaski - University of Delaware/ Nemours* (fkubaski@udel.edu) -- *Young Investigator Grantee*

- Mucopolysaccharidoses (MPSs) are progressive disorders where early diagnosis allows early treatment that provides better outcomes and prognosis. We have developed a pilot study using dried blood spots (DBS) from 2640 random newborn samples and 13 newborn MPS samples. All DBS were evaluated by liquid chromatography tandem mass spectrometry to determine levels of heparan sulfate (0S, NS) and keratan sulfate (mono-KS, di-KS and ratio di-KS/total KS). Cutoffs were established for HS to diagnose MPS I, II and III. HS-0S showed 98% specificity and 77% sensitivity and it is a potential biomarker for newborn screening of MPSs.

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**Tuesday 3:00 PM**
**Poster #8 in Exhibit Hall**

**Translational Research Workflows on LC-HRAM Platform for Detection of Pathogen Induced Cancer in Human T-Cell Leukemia Virus Type 1 Disease**

*Sucharita Dutta - EVMS* (sucha227@gmail.com)

- Exosomes are micro vesicles secreted by the cell membrane and their contents could be used as an effective means to detect many different cancers. By profiling the Exosome cargo from blood samples of patients from different stages of Leukemia we are exploring for Leukemia specific biomarkers that are secreted into the blood. An integrated profiling of the microRNA, messengerRNA and protein content of the exosome would lead to unique signatures that make exosomes ideal for cancer detection. Here, we review the unique proteomic contents of exosomes originating from Leukemia cancer cells as well as their functional effects to promote tumor progression.

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**Tuesday 5:00 PM**
**Poster #9 in Exhibit Hall**

**Cleanert HFMF® A New Sample Clean-up Technique for Plasma Sample Prior to LC-MS/MS in Bio-analysis**

*Warren Chen - Bonna-Agela Technologies* (xiaohua_chen@agela.com.cn)

- Plasma represents a major sample form in bio-analysis. The major challenge in the preparation of plasma samples prior to LC-MS/MS is to remove both proteins and phospholipids. This article introduces a new sample pretreatment technique by utilizing Cleanert HFMF® hollow fiber membrane filtration®, a hollow fiber membrane grafted with cyclic acid to filtrate proteins and phospholipids by centrifugation. A comparison study between Cleanert HFMF, PPT, LLE and SPE was carried out in terms of the efficiency to eliminate the matrix effects of proteins and phospholipids. The results showed HFMF enjoys the best capacity for removing the major impurities in plasma.
Targeted Protein Quantification from FFPE Tumor Tissue Using Mesodissection and Liquid Tissue SRM Assay: Comparison to a Laser Microdissection Platform

Chao Gong - NantOomics (chao.gong@nantomics.com)

- Many oncology therapies target specific proteins; therefore, technologies to quantify tumor-specific protein targets are required. Our current platform uses laser-assisted microdissection to isolate and collect tumor cells for analysis from FFPE tissues mounted on DIRECTOR® slides. However, sections cut onto glass microscope slides are often the only materials available, limiting the utility of high resolution laser microdissection. In this study, we present the evaluation of a tissue mesodissection platform to effectively dissect tumor cells standard glass slides, followed by Liquid Tissue® SRM assays to simultaneously quantify 26 protein biomarkers. Quantitative results from mesodissection and laser microdissection are compared.

Rapid and Sensitive Analysis of a 93-Compound Forensic Panel in Urine

Xiang He - SCIEX (xiang.he@sciex.com)

- In this poster, we describe a rapid and sensitive analysis of a comprehensive forensic compound panel in human urine using ExionLCTM AC and QTRAP®/Triple QuadTM 4500 LC/MS/MS system. This forensic panel contains 93 compounds with both ionization polarities therefore the method involves fast polarity switching. There are a total of 212 MRM transitions in the method; monitoring 2 transitions per analyte and 1 transition for each internal standard used and the total LC runtime is 6.5 minutes (can be shortened for smaller panel). Sample preparation is based on enzymatic hydrolysis and a simple “dilute and shoot” methodology.

Quantification via Signature Peptides: The Advantage of Using Differential Ion Mobility Spectrometry

Evgueni Fedorov - Biotrial Bioanalytical Services (evgueni.fedorov@biotrial.com)

- Some bioactive peptides and proteins exhibit their activity at very low concentrations. Selective and sensitive assays are also required for biomarkers. Although signature peptides are often used to increase the sensitivity in LC-MS/MS determination of large molecules, there is a risk that isobaric interferences might be accounted for the target compound. The use of Differential Ion Mobility Spectrometry (DMS) as an additional separation dimension helps to increase selectivity and specificity. The SelexION™ option with 6500 triple quadrupole mass spectrometer from Sciex permitted to remove endogenous interferences and achieve an LLOQ of 5 pg/mL in LC-MS/MS method for Exenatide, a GLP-1 receptor agonist.

Validation of an Algorithm for Determining Urinary Medication Cutoffs Using Quantitative LC-MS/MS

Amadeo Pesce - UCSD (pesceaj@ucmail.uc.edu)

- The advent of quantitative methods of determining medications and their metabolites in urine using LS-MS/MS analysis presents a quandary of establishing an appropriate cutoff to assess medication compliance. We suggest a simple frequency distribution plot after log transformation will make the data approximately Gaussian. Extrapolation of the lower values allows estimate of a 2.5% cutoff. Quantitative urinary excretion of hydrocodone (734 patients) and hydromorphone (732) were evaluated. Values less than 20ng/mL were excluded. The frequency distribution plot of hydrocodone roughly followed a Gaussian distribution with an estimated 2.5% cutoff of 20ng/mL. However, the hydromorphone was not Gaussian.
A Multiplexed LC-MS/MS Method for Quantitative Analysis of Apolipoproteins in High-Density Lipoprotein

Robin Thomas - University of Minnesota (rmkarras@umn.edu)

- High-density lipoprotein (HDL) consists of many apolipoproteins which play important roles in regulation of cholesterol transportation. Elevated cholesterol is a well-established risk factor for cardiovascular diseases. Individuals with cardiovascular risk factors have an increased risk of developing Alzheimer's disease (AD); however cholesterol-lowering therapies do not appear to reduce AD risk. An analytical method to allow quantitative analysis of HDL will allow future investigation of HDL apolipoproteins as therapeutic targets for AD. We isolated HDL fractions in plasma specimens using ultracentrifugation. Following trypsin digestion, the fractions were assayed using LC-MS/MS, and quantified using peptide standard curves. Four HDL proteins (Apo-A1, Apo-A2, Apo-C2, and Apo-C3) were compared to immunoassay results with three indicating correlation.

Utility of Suspect Screening by High Resolution Mass Spectrometry: Adulterated Xanax

Xander van Wijk - University of California, San Francisco (Xander.VanWijk@ucsf.edu) -- *Young Investigator Grantee*

- A series of patients in the San Francisco Bay Area were treated for complications after ingesting counterfeit Xanax tablets purchased illegally off the street. Serum, urine, and two counterfeit tablets were analyzed using a previously validated method on an ABSciex TripleTOF®5600 system. Targeted analysis, i.e. analysis by known accurate mass, retention time, isotope and fragmentation pattern, revealed the presence of fentanyl in these tablets and biological samples. Suspect analysis, i.e. analysis by exact mass and theoretical isotope pattern, preliminary identified etizolam, a non-FDA approved benzodiazepine analog. Presence of etizolam was later confirmed using a reference standard. This case exemplifies the utility of suspect analysis in clinical toxicology by preliminary identification of a compound that was not identified by targeted analysis.

A Split Hair Comparison of Human Hair Cortisol Levels Using an Immunoassay versus Liquid Chromatography-Mass Spectrometry

Howard Horng - University of California, San Francisco (Howard.Horng@ucsf.edu) -- *Young Investigator Grantee*

- Measuring hair cortisol levels in humans to determine long term systemic exposure is increasingly being used as a biomarker of chronic stress. Since human hair has a fairly uniform growth rate (~1 cm/month), one can investigate periods of time in which stress is absent, present, or most pertinent. The objective of this study was to develop and validate an LC-MS/MS method for the measurement of cortisol in hair and compare the method to the Siemens Centaur cortisol competitive immunoassay.

Paper Spray-tandem Mass Spectrometry for Therapeutic Drug Monitoring of Tacrolimus, Cyclosporin and Sirolimus in Whole Blood: What Worked and What Didn't?

Run Zhang Shi - Stanford University School of Medicine (rzshi@stanford.edu)

- Paper spray (PS) is open atmosphere ionization for direct and rapid mass spectrometry analysis. It is performed by simultaneously extracting and ionizing dried sample deposited on paper matrix. A PS-MS/MS method for TDM of cyclosporin, sirolimus, and tacrolimus was developed and evaluated. The method uses PS disposable cartridges and automated sample extraction and ionization interface (Prosolia Inc.) and TSQ Vantage tandem mass spectrometry (Thermo Scientific). Assay sensitivity, specificity, linearity, imprecision, and accuracy met set criteria. PS-MS/MS is a viable alternative to immunoassays or LC-MS/MS methods for immunosuppressive drug TDM, and its advantages and limitations discussed.
Tuesday 3:00 PM
Poster #18 in Exhibit Hall
**Reduction in Pipette Tip Consumable Cost and Waste Through Innovation**

*Ali Safavi  -  Grenova (asafavi@grenovasolutions.com)*

- As the number of samples processed in labs using high-throughput processes has increased, there has been a corresponding rise in the level of waste, such that in 2010, four million pounds of plastic pipette tips were disposed of after just one use. The TipNovus high-throughput automated pipette tip cleaning system from Grenova enables laboratories to safely reuse sanitized tips and thereby reduce cost and waste output.

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Tuesday 5:00 PM
Poster #19 in Exhibit Hall
**Fully Automated Broad Spectrum Extraction of Drugs and their Metabolites from Oral Fluid Samples Using Narrow Bore OFX Solid Phase Extraction Columns**

*David Hall  -  SPEware Corporation (david.hall@speware.com)*

- Increasingly, clinical and toxicology laboratories are asked to analyze oral fluid samples. The ease and non-invasive nature of oral fluid collection makes it an attractive alternative to more traditional collection of urine or blood. Here, we present a process for robotic pipetting of oral fluid samples, automated extraction of the samples, online evaporation and reconstitution of the extracts (“selective elute and shoot”) and subsequent analysis of the extracts for the presence of a representative list of drugs and drug metabolites. Analyses of the extracts were performed on an AB Sciex 5000 LCMS system with focus on linearity and LLOQ measurements.

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Tuesday 3:00 PM
Poster #20 in Exhibit Hall
**Comparison of Dried Blood Spot Collection Devices by Paper Spray Ionization Mass Spectrometry**

*Karen Cesafsky  -  Purdue University (kcesafsk@purdue.edu)*

- Paper spray ionization (PS) is an emerging technique that combines sample collection, preparation and ionization on a paper substrate for rapid analysis of small analytes by mass spectrometry. Currently, there are many commercially available DBS devices that may be integrated with PS. Coupling PS and DBS devices eliminates the need of offline extraction of the analytes from the DBS. Additionally, with this new approach, the PS measurement may utilize specialized DBS devices for improved sample volume precision and accuracy or filtration of the biological matrix. Analytical figures of merit of DBS collection devices coupled with PS are investigated.

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Tuesday 5:00 PM
Poster #21 in Exhibit Hall
**Solid Phase Extraction Optimization and Separation of Vitamin D Metabolites by LC-MS/MS, for Clinical Research**

*Robert Wardle  -  Waters Corporation (robert_wardle@waters.com)*

- Many challenges are posed by matrix interferences when analyzing vitamin D metabolites by LC-MS/MS for clinical research. In particular, lysophosphatidylcholines (LysoPCs) cause ion suppression effects in mass spectrometry. Elution profile testing was carried out using Waters® Oasis® HLB and Oasis PRIME HLB µElution plates for the analysis of vitamin D metabolites by LC-MS/MS to optimize and compare SPE conditions to protein precipitation. Oasis PRIME HLB was shown to increase analytical sensitivity of vitamin D metabolites through the removal (>99%) of the targeted LysoPCs when compared to protein precipitation and Oasis HLB. Furthermore, the workflow created was minimal, simply load the protein precipitate, wash and elute. For Research Use Only, Not for Use in Diagnostic Procedures.
LC-MS/MS Measurements of Parathyroid Hormone-Related Protein (PTHrP): Negative Correlation Between Age and PTHrP Concentrations in CSF

Mark Kushnir - ARUP Institute (kushnmn@aruplab.com)

Parathyroid hormone related protein (PTHrP) is involved in intracellular calcium regulation. Calcium is necessary for the nerve signaling and brain function, but limited information is available related to PTHrP expression in brain. Recently we developed LC-MS/MS method for the assessment of PTHrP in plasma. Using this method we analyzed PTHrP in a set of paired serum and CSF samples, and evaluated distribution of PTHrP concentrations, and the ratio of concentrations (PTHrP_{CSF}/PTHrP_{serum}) in adults. A trend to higher PTHrP concentrations with increasing age was observed in serum, while a trend to lower concentrations was observed for PTHrP_{CSF} and the PTHrP_{CSF}/PTHrP_{serum} ratio.

Advances in Solid Phase Extraction – Removal of Residual Phospholipids Using a Novel Reverse-phase Sorbent

Jonathan Danaceau - Waters Corporation (jonathan_danaceau@waters.com)

A novel reversed-phase SPE sorbent has been developed that is designed to additionally remove phospholipids from biological samples. Pretreated samples were loaded directly onto the SPE sorbent without conditioning and equilibration. The three-step protocol (load-wash-elute) eliminated >95% of phospholipids compared to protein precipitation. This reduction was shown to have direct impacts on ion suppression of co-eluting analytes.

Characterizing Secreted Factors Contributing to Drug Resistance in Pancreatic Cancer Tumor Micro-Environment

Matthew Rosenow - Translational Genomics Research Institute (mrosenow@tgen.org)

Poor prognosis in pancreatic cancer has largely been linked to therapeutic resistance to first-line treatments. Tumor heterogeneity in pancreatic adenocarcinoma microenvironment (consisting of fibroblasts, pancreatic stellate cells (PSC), and extracellular matrix proteins (EMPs)) may confer this resistance. Studies have implied that secreted factors targeting tumor growth and metastasis pathways may play an important role in conferring drug resistance as well as the secretion of EMPs that contribute to fibrosis and act by physically limiting drug entry. We carried out a bottom-up mass spectrometry discovery analysis on the secretome to identify secreted factors from PSCs and MiaPaCa—a pancreatic carcinoma cell line—in the presence of the chemotherapeutic drug triptolide. Highly targeted pathways were identified that may provide insight to additional therapeutic strategies or targets.

Determination of PBDEs in Human Milk by Automated Solid Phase Extraction and Gas Chromatography/High Resolution Mass Spectrometry

Weihong Guo - California Department of Toxic Substances Control (weihong.guo@dtsc.ca.gov)

Although they have been banned since 2004, PBDEs are still ubiquitous in humans and in wildlife. Due to their possible adverse health effects, biomonitoring programs and research studies require that PBDEs be continuously measured in biological matrices including breast milk, serum, and tissue. We have developed a new method to determine PBDE levels in human milk that improves throughput, precision, and that reduces background contamination. This method has been validated using breast milk samples from an epidemiological study with high, medium, and low PBDE levels measured previously using the traditional method. PBDE levels from the two methods are in agreement.
A Novel Integrated LC-MS/MS Strategy for the Ultra-sensitive Determination of Catecholamines in Human Peripheral Blood Mononuclear Cells (PBMC)

Xiaoguang (Sunny) Li - Pharmasan Labs (xiaoguang.li@pharmasan.com)

We develop and validate the first LC-MS/MS method for determination of catecholamines in human peripheral blood mononuclear cells (PBMC). The analytical novelty includes the first solid phase extraction on a 96-well hydrophilic-lipophilic-balanced microplate upon complexation with phenylboronic acid, optimal LC condition and MRM summation, allowing simultaneous quantitation of catecholamines with ultra-sensitivity at 1–5 pg/mL without requiring derivatization and evaporation. Satisfactory validation results and successful assessment of reference intervals (n = 40) suggested good reproducibility and reliability of the assay. The novel approach, being simple, rapid, sensitive and reliable, will facilitate better understanding of the new arena of neural-immune network.

Targeted SPE-UPLC-MS/MS Analysis of Oxylipins: from Profiling to Quantification for Translational Research Studies

Billy Molloy - Waters Corporation (billy_molloy@waters.com)

Oxylipins are signaling molecules that play a role in the regulation of many key biological processes, most notably inflammation. Here, we describe targeted, quantitative SPE-UPLC-MS-MS assays for the analysis of various oxylipins subsets and classes. These subsets represent down-stream products or oxylipins from particular metabolic pathways. Matrix samples were prepared using mixed mode OASIS MAX µElution SPE and analysed using an ACQUITY UPLC I-Class system interfaced to a Xevo TQS Micro Tandem Quadrupole Mass Spectrometer. We demonstrate these methods to be sensitive, selective, linear and precise and therefore suitable for use in translational research studies.

Multi-Modal Mass Spectrometry Imaging for Clinical and Biomedical Research Applications – a Comparison of MALDI and DESI Techniques for Tissue Imaging

Emanuelle Claude - Waters Corporation (emmanuelle_claude@waters.com)

Mass spectrometry imaging (MSI) is now increasingly used for clinical research applications due to significant technological improvements that have made the technique more accessible. MALDI, initially introduced by Caprioli et al., is the dominant MSI technique used today, due to the ability of MALDI to analyse proteins and also its widespread commercial availability. In the last few years, several alternative ambient ionization techniques have been developed that can ionize clinically important molecules such as lipids directly from tissue. One of these techniques, desorption electrospray ionization (DESI), requires minimum sample preparation and is therefore more compatible within a clinical research environment. Here we compare and contrast these two imaging techniques which can be operated on an oa-QTOF mass spectrometer.

Harmonization in Individual Bile Acids Analysis in Mouse and Man – an Inter-Laboratory Ring Trial, Method Comparison and Clinical Relevance of Bile Acids

Maria Chiam - Biocrates Life Sciences AG (maria.chiam@biocrates.com)

Interest in bile acids has been growing since the discovery of their significance, hormone-like regulatory factors acting via nuclear-farnesoid-X receptor (FXR), and G-protein-coupled plasma-membrane bound receptors (TGR5). Therefore, simultaneous quantitation of individual bile acids is of highly interest in many diseases, life-style, and clinical-related questions e.g. in nutrition, use of antibiotics, gut microbiome, metabolic syndrome, type 2 diabetes, Alzheimer’s disease, NAFLD or other liver related diseases. Standardization is mandatory to develop bile acid related biomarkers and to bring it into clinical routine application. Here, we describe the world-wide first bile acid assay in standardized format and will present the inter-laboratory ring trial data, method comparison and discuss their clinical relevance.
Tuesday 5:00 PM
Poster #31 in Exhibit Hall

Sensitive and Specific LC-MS/MS Analysis of Plasma Free Metanephrines Using Either On-line or Off-line Sample Cleanup

Katharina Kern - RECIPE Chemicals + Instruments GmbH (k.kern@recipe.de)

- RECIPE's CE IVD certified ClinMass® LC-MS/MS Complete Kits – Free Metanephrines in Plasma allow quantitation of metanephrine, normetanephrine and 3-methoxytyramine in human plasma after on-line or off-line sample preparation. Both kits include simultaneous extraction and concentration, while the separation and mass selective detection is achieved using LC-MS/MS. The method shows outstanding validation results for all analytes. Close agreement of analyte concentrations with results reported for RCPAQAP proficiency testing scheme could be obtained. With RECIPE’s MS11000/MS11100 a fast, easy and reliable analysis of plasma free metanephrines has been realized which is very well suited for clinical routine analysis.

Tuesday 3:00 PM
Poster #32 in Exhibit Hall

Direct Injection of Serum and Online Solid Phase Extraction for the Quantification of Antidepressants by Liquid Chromatography Tandem Mass Spectrometry

Claudio De Nardi - Thermo Fisher Scientific (claudio.denardi@thermofisher.com)

- An analytical method for the quantification of 14 tricyclic antidepressants based on direct injection of human serum is reported. The method involves automated addition of the internal standards followed by injection of the serum sample onto an online SPE liquid chromatographer using a Thermo Scientific™ Transcend™ II system. Mass spectrometric detection is performed by single reaction monitoring on a Thermo Scientific™ TSQ Endura™ triple quadrupole using heated electrospray ionization. The method was analytically validated using the MS9050 ClinMass® TDM Platform from RECIPE with the MS9150 Add-On Set for Tricyclic Antidepressants and limit of quantification, linearity range, accuracy and precision were evaluated.

Tuesday 5:00 PM
Poster #33 in Exhibit Hall

A Novel 6x5 Peptide Mixture for Full Instrument Characterization and Performance Monitoring

Michael Rosenblatt - Promega (mike.rosenblatt@promega.com)

- Clinical mass spectrometry requires robust instrument performance. Currently, as both low and high-resolution instruments are being utilized to carry out clinical tests, a standardized reagent is needed for system suitability monitoring. In this study we present a full workflow for the analysis of HPLC, MS1 and MS2 instrument stages using a peptide mixture of isotopologues that span 4 orders of dynamic range. The HPLC and MS1 data were analyzed using PReMiS™ software which reports directly on critical LC and MS1 parameters. For the MS2 evaluation, both SRM (Triple-stage-Quadrupole) and PRM (high-resolution orbitrap) data were analyzed with Skyline to analyze MS/MS related metrics associated with both types of instruments.

Tuesday 3:00 PM
Poster #34 in Exhibit Hall

A Novel Liquid Chromatography Mass Spectrometry Method for the Analysis of Succinate: Fumarate Ratios in the Detection of SDHx-associated Tumours

Talia Novos - Prince of Wales Hospital, SEALS (talia.novos@hotmail.com) -- *Young Investigator Grantee*

- Paragangliomas and pheochromocytomas are endocrine tumours associated with mutations of the Succinate dehydrogenase (SDH) gene. SDH catalyses the conversion of succinate to fumarate in the Krebs cycle. Therefore a mutation in the SDHx gene will result in an accumulation of succinate and decreased production of fumarate. We have developed a novel method for the analysis of these metabolites by liquid chromatography mass spectrometry. Increased succinate:fumarate ratios correlate with patients that have been confirmed to have SDHx mutations with immunohistochemistry staining. This method will aid in the early detection of patients at risk of developing SDHx associated tumours.
Tuesday 5:00 PM
Poster #35 in Exhibit Hall
A New Strategy for the Detection of the Family of Benzophenone-3 Structurally Related Compounds and their Metabolites in Human Urine Samples
Yu-Chen Chang - California Department of Public Health (yu-chen.chang@cdph.ca.gov)

• A sensitive method for testing urinary concentrations of benzophenone-3 (BP-3) developed by our laboratory is routinely used in biomonitoring studies. In this presentation, we describe a new strategy to expand the testing panel to the family of structurally-related compounds using BP-3 as a model system. BP-3 and its analogs are used in personal care products, such as sunscreens, as well as food packaging, etc., to protect the skin and products from UV light. As some of these chemicals have carcinogenic, endocrine disrupting, or developmental or reproductive toxicity, wide exposure to vulnerable populations, particularly women and infants, present potential health concerns.

Tuesday 3:00 PM
Poster #36 in Exhibit Hall
A Dilute-And-Shoot Method for Simultaneous Analysis of Vanillylmandelic Acid, Homovanillic Acid and 5-Hydroxyindoleacetic Acid in Human Urine
Shun-Hsin Liang - Restek Corporation (shun-hsinliang@restek.com)

• Vanillylmandelic acid (VMA), homovanillic acid (HVA), and 5-hydroxyindoleacetic acid (5-HIAA) are final metabolites of epinephrine, dopamine, and serotonin, respectively. Measurement of these metabolites in urine is used for the diagnosis of carcinoid and neuroendocrine tumors including neuroblastoma, pheochromocytoma, and paraganglioma. The development of a simple dilute-and-shoot and yet accurate, specific, and fast LC-MS/MS analysis would greatly reduce the time and cost for this type of clinical test. Using a Raptor™ Biphenyl column, it was demonstrated that VMA, HVA, and 5-HIAA can be simultaneously analyzed in human urine without extensive sample clean up and resulted in accurate and reproducible quantitation.

Tuesday 5:00 PM
Poster #37 in Exhibit Hall
Identification of Nontuberculous Mycobacteria Species by Tinkerbell LT
Jae-Seok Kim - Hallym University (jaeseokcp@gmail.com)

• NTM species identification is important for the appropriate treatment of corresponding type and its clinical significance. In this study, 63 species of mycobacteria reference strains and 105 clinical isolates, identified by multi-locus sequencing, were analyzed by MALDI-TOF MS (Tinkerbell LT, ASTA, Suwon, Korea). We acquired specific signals of each individual mycobacterial species cultured on 3% ogawa and MGIT on the basis of unique mass fingerprints. In addition, several mass peaks were selected as diagnostic markers for species confirmation. In conclusion, Tinkerbell LT-MS could be applied for rapid and reliable identification of mycobacteria in clinical laboratory.

Tuesday 3:00 PM
Poster #38 in Exhibit Hall
Determination of Asymmetric Dimethylarginine (ADMA) and Symmetric Dimethylarginine (SDMA) in Human Serum by Ion-Pair Chromatography-Mass Spectrometry
Haiqing Ding - Cleveland HeartLab, Inc. (hding@clevelandheartlab.com)

• Here we report a reliable LC-MS/MS method for the determination of ADMA and SDMA in human serum by ion-pair chromatography-mass spectrometry. With heptafluorobutyric acid as an ion-pair additive to mobile phases, polar molecules ADMA and SDMA can be well retained on a reversed-phase column. This eliminates the need for pre-column derivatization which is time consuming. Baseline separation of ADMA from SDMA can be easily achieved compared to normal-phase chromatography. The method was validated on an Agilent multi-stream LC-MS/MS System. The method provides not only good linearity, accuracy, and precision, but also increased productivity with the use of multi-stream LC system.
Peace of Mind in the Era of LDT Regulation - A Home-brew Barcoding Solution for Tracking Everything LC-MS/MS

Krista Pratico - UCSD Center for Advanced Laboratory Medicine (kpratico@ucsd.edu)

With regulation of LDTs on the horizon, the need for laboratories to develop a feasible method of logging LC-MS/MS reagents and solvents is inevitable. Such a system must be able to document and track all lot changes and lend itself to retrospective troubleshooting when the components of a prepared solvent or reagent cause subpar performance. We have developed a workflow that involves the use of individual barcodes - to document lot and expiration of reagents, track where and when they were used, and document that validation was performed - all in a MS Access database. This system can be customized to track anything in the LC-MS/MS lab - from chemicals to consumables.

In-line, Automated Method for the Sample Preparation and LC-MS/MS Analysis of Dried Matrix Blood Microsamples for Immunosuppressant Drug Monitoring

Erik Ruijters - MagnaMedics Diagnostics B.V. (eru@magnamedics.com)

LC-MS/MS is replacing HPLC and immunoassays for immunosuppressant drug monitoring to achieve greater sensitivity and specificity. This study evaluated an in-line LC-MS/MS method where 10 µL blood samples collected by a microsampling device (Mitra) were prepared for analysis using a process (MagSi-TDMPREP) to eliminate interferences. Automation of this method resulted in a processing time of 30-45 minutes for 96 samples, robot dependent (4 or 8 span), while resulting in ≥ 80% recovery (RSD <15%) for four immunosuppressants. This method also included the tools required to handle, track, and prepare samples for direct LC-MS/MS injection or batching in vials/microtiter plates.

Simultaneous Therapeutic Drug Monitoring for Voriconazole, Posaconazole, Fluconazole, Itraconazole, and Metabolites in Human Serum by HPLC-MS/MS

Yi Xiao - Children’s Hospital Los Angeles (yxiao@chla.usc.edu) -- *Young Investigator Grantee*

A simple and fast sample extraction and HPLC-MS/MS method was developed for simultaneous quantitation of voriconazole, voriconazole-N-oxide, posaconazole, fluconazole, itraconazole, and hydroxyitraconazole in human serum for therapeutic drug monitoring of antifungal treatments. Sample preparation involves only protein precipitation and dilution; LC-MS/MS method takes only three minutes. The inter-day CVs ranged from 4% to 6%, and the intra-day CVs ranged from 2% to 4%. The recoveries were between 95% and 103% for three concentrations tested. This method is accurate and robust, and offers a cost-effective tool for dosing adjustment for single-drug antifungal regimens and combination salvage therapies on a daily basis.

Pain Panel Drug Screening by Nanopost Array Laser Desorption Ionization Mass Spectrometry (NAPA LDI-MS) on REDichip

Christopher George - Protea Biosciences, Inc. (christopher.george@proteabio.com)

REDIchips are comprised of nanopost arrays (NAPA), fabricated on silicon substrates to form patterned targets for high throughput LDI-MS of small molecules in MALDI instruments. The REDichip’s NAPA targets exhibit excellent performance for quantitation and screening of pain panel drugs such as opiates/opioids, anesthetics, and cocaine metabolites in biofluids. The pain drugs are quantitated over at least four orders of magnitude dynamic range to determine appropriate cut-off values for pass/fail parameters for drug screening from a variety of human biofluids. REDichip’s NAPA LDI-MS workflow allows for efficient and sensitive detection and quantitation of several classes of pain drugs.
Tuesday 3:00 PM
Poster #44 in Exhibit Hall
**An Ion Mobility Screening Approach for the Detection of Toxicologically Relevant Substances**
*Jeff Goshawk - Waters Corporation (jeff_goshawk@waters.com)*

- The utility and potential benefit of collision cross-section (CCS) data, as generated through use of ion mobility separation (IMS) techniques, was evaluated for >50 toxicologically-relevant substances. Solvent standards were analysed using an established UPLC-method in combination with an IMS-QTof (Waters). Reference CCS values were measured and then incorporated into an existing toxicology library comprising retention time and exact mass data. Collision cross-section measurements were shown to be highly reproducible (within 2% of reference), both in the presence or absence of biological matrix. Use of IMS led to cleaner, low and elevated energy spectra due to the alignment of ions in drift time. CCS values provide an additional dimension of specificity which proves valuable in systematic toxicological analysis.

Tuesday 5:00 PM
Poster #45 in Exhibit Hall
**Automated Comprehensive Urine Sample Preparation Using DPX Extraction on the Hamilton NIMBUS96 with LC-MS/MS Analysis**
*Kaylee Mastrianni - University of South Carolina (mcdonakr@email.sc.edu)*

- A high throughput sample preparation method for drugs of abuse (38 compounds) in urine was developed using DPX tip technology coupled with the Hamilton NIMBUS96 robotics system. The sample preparation of two well plates of 96 hydrolyzed samples takes approximately 15 minutes to complete for LC-MS/MS analysis. The method was evaluated for linearity, precision, extraction efficiency, and limits of detection and quantitation. The method established herein is highly reproducible and provides the necessary sensitivity for forensic and clinical purposes.

Tuesday 3:00 PM
Poster #46 in Exhibit Hall
**Interferences of Blood Collection Tubes in the Measurement of Androgen Concentrations After Administration of a Novel Androgen Ester**
*Jonas Ceponis - Los Angeles Biomedical Institute at Harbor-UCLA (jceponis@labiomed.org) -- *Young Investigator Grantee*

- Our aim was to determine the most appropriate blood collection tube for measurement of DMAU and DMA in blood after oral administration of Dimethandrolone Undecanoate (DMAU), a new androgen being developed as a potential male hormonal contraceptive. In vitro experiment showed that when venous blood was transferred into six types of blood collection tubes and known amounts of DMAU were added to each tube, NaF+Oxalate, NaF+EDTA and P800 tubes showed the least interference in measuring DMA when kept for 30 min at 4C. In vivo experiment in 6 subjects showed that when serial blood samples were collected over 24h after oral administration of DMAU and kept for 30 min at 4C, DMA level differences between the different blood collection tubes were within the imprecision of the assays. The pronounced interference seen in vitro was not reflected in samples collected after oral administration of DMAU.

Tuesday 5:00 PM
Poster #47 in Exhibit Hall
**The Application of Ion Mobility Mass Spectrometry to Lipidomics – a Demonstration of Instrumental Capabilities for a Diabetic Mouse Model**
*Julia Denes - University of Cambridge (jd740@cam.ac.uk)*

- The use of ion mobility coupled with high resolution LC-MS/MS has been applied to investigate the lipidomic changes in blood plasma for a mouse model of type 2 diabetes. The ability to separate ions across four dimensions (retention time, mass to charge ratio, fragmentation, ion mobility) has allowed us to improve detection of lipid species obtained from a complex matrix. In addition, multiplexing and all ion fragmentation were applied to increase sensitivity and selectivity of the analysis. Phospholipid distribution of plasma samples from diabetic mice model was compared with controls and significant differences were identified. Identification of biomarkers and differentiation of structural isomers was facilitated by collisional cross section data. Results clearly show the potential of the technique in the field of lipidomics.
Tuesday 3:00 PM
Poster #48 in Exhibit Hall
**Uromics: Metabolomics in Urine for Seroquel®, Latuda®, and Haldol®**
*Erin Strickland* - Ameritox, Ltd. (erin.strickland@ameritox.com)

* Metabolomic studies of drugs in the body customarily focus on blood samples to identify these compounds.
* Metabolomic studies in urine (e.g., uromics) are less common. Using an exact mass LC-QTOF instrument and enzymatic hydrolysis, as needed for confirmation, work in this lab has identified metabolites of a variety of antipsychotic drugs in urine that were either not previously identified in the literature or were known but thought to be minor metabolic pathways. This work will specifically report on advances in Seroquel®, Haldol®, and Latuda® monitoring demonstrating both new metabolites and increased importance of known metabolites.

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Tuesday 5:00 PM
Poster #49 in Exhibit Hall
**An Improved Tandem Mass Spectrometry Method for GALC Enzyme Assay and Psychosine Analysis in Dried Blood Spots for Identification of Krabbe Disease**
*Hsuan-Chieh Liao* - University of Washington (liaohc6@uw.edu) -- *Young Investigator Grantee*

* Krabbe disease is an inherited autosomal recessive disorder caused by mutations in the GALC gene. Deficiency in GALC results in an abnormal accumulation of a highly cytotoxic metabolite, called psychosine. Our lab has developed mass spectrometry methods that are being used in newborn screening (NBS) of lysosomal storage diseases. Now we focus on high accuracy GALC enzyme assays using purified white blood cells from patients suspected to have Krabbe disease. Psychosine measurement in dried blood spots and cerebrospinal fluid were also developed and could serve as a second tier assay. The methods should reduce the false positive rate of NBS and help determine disease severity and monitor Krabbe patients.

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Tuesday 3:00 PM
Poster #50 in Exhibit Hall
**Mass Spectrometry Imaging of Biological Tissue Sections and Small Cell Clusters on Nanophotonic Laser Desorption Ionization Substrates**
*Sylwia Stopka* - The George Washington University (stopka@gwmail.gwu.edu) -- *Young Investigator Grantee*

* Mass spectrometry imaging (MSI)-based techniques provide versatile spatially-resolved chemical information directly from tissues. Matrix-assisted laser desorption ionization is the dominant technique in MSI, but due to the narrow dynamic range of quantitation and the spectral interferences, it is poorly suited for the MSI of small molecules. Here we present the first evidence for a new matrix-free MSI technique using nanophotonic laser desorption ionization (LDI) from a silicon nanopost array (NAPA). In mouse brain and kidney, over ions were mapped and correlated to anatomical features. Additionally, human and microalgae cells were cultured and analyzed on these silicon substrates, allowing correlation of cell number within a given pixel to the corresponding ion intensities. These results demonstrate the utility of LDI-MSI from NAPA for tissue sections and small cell population analysis.

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Tuesday 5:00 PM
Poster #51 in Exhibit Hall
**Bioanalytical UPLC-MS/MS Method Development and Validation for Measuring Most Commonly Used Antimicrobials in England from Human Blood Plasma**
*Karin Kipper* - St. George’s, University of London (karin.kipper@gmail.com)

* Bioanalytical UPLC-MS/MS method was developed and validated for the most commonly used antimicrobials in England’s intensive care units. The list of the antimicrobials consisted: co-amoxiclav (amoxicillin with clavulanic acid), piperacillin with tazobactam, fluclaxacillin, meropenem, etrapenem, ceftriaxone, cefotaxime, benzylpenicillin, clarithromycin and fluconazole. The separation between the compounds was obtained with reversed phase chromatography using the weak ion-pairing agent hexafluoroisopropanol and basic pH (9.5). The method was fully validated - stability, matrix effects, accuracy, precision, linearity, limits of quantification and method’s uncertainty estimation was evaluated.
Tuesday 3:00 PM
Poster #52 in Exhibit Hall

New Approach for Intact Protein Separation, Detection, and Quantitation Based on Multiple Reaction Monitoring Triple Quadrupole Mass Spectrometry

Evelyn Wang - University of Texas at Arlington (evelyn.wang@mavs.uta.edu) - *Young Investigator Grantee*

- There is an increasing demand for protein quantitation in biological fluid for disease detection, protein therapeutics monitoring, and response control during clinical trials. Current triple quadrupole mass spectrometer (QQQ-MS) protein quantitation methods require protein digestion step that is often incomplete thus introduce error. Our method bypasses protein digestion to directly quantify intact proteins on QQQ-MS with multiple reaction monitoring. A series of model proteins are shown to be sensitively and specifically detected, even in the presence of biological matrices. A chromatographic method was developed to address the complex biological matrix for this system. The success of this project can aid clinical diagnostic and treatment advancements.

Tuesday 5:00 PM
Poster #53 in Exhibit Hall

Development of Reference Measurement Procedure for 24R,25-Dihydroxyvitamin D3 and Value Assignment on SRMs of Vitamin D Metabolites in Human Serum

Susan Tai - National Institute of Standards and Technology (susan.tai@nist.gov)

- Accurate and precise quantitative evaluations of 24R,25-dihydroxyvitamin D3 (24R,25(OH)2D3) are important for reliable diagnosis and appropriate treatment of diseases. 24R,25(OH)2D3 is an important vitamin D metabolite used as a catabolism marker and indicator of kidney disease. NIST has developed a candidate RMP for the determination of 24R,25(OH)2D3 in human serum using ID-LC/MS/MS. This method of high precision and high accuracy was used to value assign the concentrations of 24R,25(OH)2D3 in 2 SRMs of Vitamin D Metabolites in Human Serum (SRM 972a and candidate SRM 2973), which can serve as an accuracy base for the routine methods used in clinical laboratories.

Tuesday 3:00 PM
Poster #54 in Exhibit Hall

Results from a Seven Month Trial of Single Point Calibration

Geoffrey Rule - ARUP Laboratories (geoffrey.s.rule@aruplab.com)

- We have evaluated the potential for use of a single point calibration over a period of seven months and a total of 340 analytical runs using production laboratory data. The single point calibration data is incorporated into a weighted response factor that provides a more stable estimate of instrument response and therefore better analytical precision. This is shown for three androgen analytes along with several observations that were made over the seven month period. The weighted response factor is shown to behave in a predictable fashion. Several points to consider in adoption of this type of strategy are discussed.

Tuesday 5:00 PM
Poster #55 in Exhibit Hall

Quantifying Translational Differences Between Single Blastomeres in the 16-cell Xenopus Embryo by Mass Spectrometry

Camille Lombard-Banek - The George Washington University (clombard@email.gwu.edu) - *Young Investigator Grantee*

- Characterization of the proteomic machinery underlying cell differentiation promises to elevate our understanding of the normal and impaired development of the vertebrate embryo. However, this requires specialized, highly sensitive tools, particularly based on mass spectrometry, to measure single cells. Here, we utilize a custom-built capillary electrophoresis microelectrospray mass spectrometry technique to study proteomic differences between selected blastomeres that were extracted from the 16-cell normal frog embryo. This technology enabled the reproducible quantification of ~150 nonredundant proteins, which allowed us to uncover translational differences between multiple blastomere types. These results set the stage for translational studies where the hindrance of developmental pathways is suspected to lead to inborn defects in the embryo.
Tuesday 3:00 PM
Poster #56 in Exhibit Hall
**Evaluation of a New Four-Channel LC and a Mass Spectrometer for Open-Access Analysis of Multiple Drug Classes in Clinical Research**

**Kristine Van Natta** - Thermo Fisher Scientific (kristine.vannatta@thermofisher.com)

- To evaluate performance of a new four-channel LC systems we developed short, efficient methods optimized for different classes of compounds including antipsychotics, antibiotics, anticonvulsants, immunosuppressants, antiarrhythmics, and antidepressants in plasma, serum or blood. The methods were implemented on a new 4-channel LC interfaced to a triple quadrupole mass spectrometer. Each LC channel ran a method optimized for a specific group of compounds. This enabled fast, open access style analysis of any group without having to change or re-equilibrate LC columns or mobile phases. The system performance evaluation was assessed by obtaining overall system productivity and also LOQ, precision and matrix effects for individual methods. Stability of the calibration curve over time was also investigated to evaluate open access functionality.

Tuesday 5:00 PM
Poster #57 in Exhibit Hall
**Development of a Sensitive, Accurate and Robust LC/MS-based Method for Profiling of Angiotensin Peptides in Plasma of Atherosclerotic ApoE-/-/LDLR-/- Mice**

**Mariola Olkowicz** - Medical University of Gdansk (m.olkowicz@gumed.edu.pl) -- *Young Investigator Grantee*

- The aim of this study was to develop an analytical methodology for accurate quantification of angiotensins: Ang I, Ang II, Ang-(1-7), Ang III and Ang IV in plasma of atherosclerotic mice. A triple quadrupole mass detector equipped with chip-based nanospray source connected to nanoHPLC was used. Plasma angiotensin profile was substantially modified in ApoE/LDLR double knock-out mice with increase in concentration of Ang II from 37.6 ± 21.3 pg mL⁻¹ in WT to 200.2 ± 47.6 pg mL⁻¹. Concentrations of Ang I, III and IV were also elevated 3-10 fold in ApoE-/-/LDLR-/- mice while that of Ang-(1-7) was unchanged.

Tuesday 3:00 PM
Poster #58 in Exhibit Hall
**Parallel Reaction Monitoring and Selected Reaction Monitoring Exhibit Comparable Quantitative Performance in Clinical Research and Forensic Applications**

**Xiaolei Xie** - Thermo Fisher Scientific (xiaolei.xie@thermofisher.com)

- Selected reaction monitoring (SRM) has emerged as the MS "gold-standard" for targeted quantification. An alternative quantitative method is parallel reaction monitoring (PRM). In PRM, the third quadruple of a triple quadrupole is substituted with a high resolution mass analyzer to permit parallel detection of all product ions in one high resolution mass analysis. Here, we evaluate the analytical performance of the PRM method and draw a comparison to SRM. We demonstrated comparable quantitative performance between PRM and SRM in terms of run-to-run reproducibility, matrix effects, and measurement accuracy using epi-vitamin D quantitation in plasma and barbiturate measurement in urine.

Tuesday 5:00 PM
Poster #59 in Exhibit Hall
**Quantitative Mass Spectrometry Imaging of Chemotherapeutics in Tissue Sections Using IR-MALDESI**

**Mark Bokhart** - North Carolina State University (mtbokhar@ncsu.edu) -- *Young Investigator Grantee*

- Infrared matrix-assisted laser desorption electrospray ionization (IR-MALDESI) mass spectrometry imaging (MSI) is a powerful analytical platform for the visualization of analyte distributions within tissue sections. Recent method development and optimization extended the analytical capabilities of IR-MALDESI MSI to provide quantitative images of xenobiotics in tissue sections. In this work, we present quantitative MSI for novel poly-2-oxazoline (POx) polymeric micelle formulations of paclitaxel (PTX) in a mouse model. The concentration and distribution of PTX in tumor, spleen and liver was determined using MSI with concentrations validated with LC-MS/MS analysis of serial sections.
Multichannel Optimization of a New Four Channel HPLC with a Single Mass Spectrometer to Simplify Workflow Complexity and to Improve Throughput of LC-MS

Jason Lai - Thermo Fisher Scientific (jason.lai@thermofisher.com)

› There are four things that matter the most to routine clinical lab operation: the quality of test results, the efficiency of generating those results, the turn-around time to report the results and how much it costs to do all this. Currently, clinical laboratories are facing challenges in handling a large number of samples with crowded lab space and shortage of experienced staff. We address clinical labs’ concerns for speed, efficiency, flexibility and laboratory space restrictions with a compact four-channel HPLC, tandem mass spectrometry and software that streamlines LC-MS workflow. For in vitro diagnostic use. Not available in all countries.

Profiling Thyroid Hormones by LC/MS/MS Analysis in Various Preclinical Species and Humans

Lina Luo - Pfizer Inc (lina.luo@pfizer.com)

› Compounds in drug development may enhance the metabolism or clearance of thyroid hormones in animal models, triggering a sequence of toxicity events, and accurate measurements of thyroid hormones are important to aid in understanding the response. In this project, we utilized a validated LC/MS/MS method to profile the five thyroid hormones (T4, T3, rT3, 3,3’-T2, and 3,5-T2) in serum samples from various animal species and humans. These results enabled us to establish the distribution in normal animals and evaluate the influence of different factors, such as gender, on the profile.

Quantitative LC-MS of Apolipoprotein L1 in Human Serum with High Throughput Automated Sample Preparation.

Shenyan Zhang - Cedars Sinai Medical Center (shenyan.zhang@cshs.org) -- *Young Investigator Grantee*

› Chronic kidney disease (CKD) is a prevalent disorder that often remains undiagnosed until its most severe renal and cardiovascular complications arise. Although biomarkers for CKD are few, Apolipoprotein-L1 variants have been directly linked to an increased risk for this disease. In order to facilitate its routine detection, we built and evaluated a quantitative LC-MS/MS assay for Apo-L1 that is compatible with automated high-throughput upstream sample preparation capable of processing 96 samples in under 6 hours.

Judging a Book by Its Data: Planning Experiments to Fully Evaluate Prospective Instrument Vendors

Thomas Laha - University of Washington (tlaha@uw.edu)

› To aid in the selection of a new mass spectrometer, we developed an experimental model which allowed the concurrent evaluation of both small molecule and peptide performance across top-tier quadrupole mass spectrometers from four LC-MS/MS vendors. Each Vendor was supplied a seven-sample test set, composed of linear admixtures of two trypsin-digested serum samples. One sample contained the human vitamin D binding globulin variant GC2 (tryptic peptide LPDATPK) and the other sample, deficient for this variant, was spiked with amphetamine to a final concentration of 150pg/mL. Vendors were asked to analyze each test mix in quadruplicate, concurrently monitoring multiple transitions for amphetamine, GC2 and GC2 internal standard. Key parameters that were compared included the y-intercept of the linear regressions, % CV at each of the concentrations, and % CV of transition ion ratios.
Tuesday 5:00 PM
Poster #65 in Exhibit Hall

**Quantitation of Serum 17-hydroxyprogesterone, Testosterone, Dehydroepiandrosterenedione and Androstenedione Using UPLC-MS/MS**

*Theresa Swift* - University of Michigan Health System (swiftt@med.umich.edu) -- *Young Investigator Grantee*

- Quantitation of steroid metabolites including 17-hydroxyprogesterone (17OHP), testosterone (TTST), androstenedione (ANDRO) and dehydroepiandrosterenedione (DHEA) is useful in the diagnosis and clinical management of adrenal disorders like congenital adrenal hyperplasia. We have developed a UPLC-MS/MS method that can be used for simultaneous measurement of 17OHP, TTST and ANDRO. DHEA was also quantified using the same sample preparation and chromatographical method but with the requirement of relatively higher sample volume. Since our method does not need a derivatization step, complete automation of the sample extraction process using a liquid handling system is feasible in the future.

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Tuesday 3:00 PM
Poster #66 in Exhibit Hall

**Quantification of Vitamin D-Binding Protein Isoforms by MRM**

*Lisa Kilpatrick* - NIST (lisa.kilpatrick@nist.gov)

- Vitamin D-binding protein (VDBP) is a plasma protein that transports vitamin D metabolites to target tissues. Recent work has shown that quantification of VDBP using immunoassays gives variable results depending on the antibody specificity; therefore, standardization of the methods used for the measurement of this protein is needed. Because there are three common isoforms, GC-1s, GC-1f, and GC-2, with up to two sites of glycosylation on the peptide unique to each isoform, quantification of the protein is challenging. In this work, a method for quantification of the three main VDBP isoforms was investigated using multiple reaction monitoring (MRM).

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Tuesday 5:00 PM
Poster #67 in Exhibit Hall

**Simultaneous Analysis of Nineteen Amino Acids in HuangQi Injection Using AQC Pre-column Derivatization and UPLC/Q-tof-MS**

*Su Zhang* - California Department of Public Health (su.zhang@cdph.ca.gov)

- It is difficult to separate, qualify and quantitate amino acids in complex matrix. A reliable method using UPLC/Q-tof-MS coupled with AQC pre-column derivatization was established to determine amino acids in Huangqi injection (a traditional Chinese injection) and its intermediates. AQC derivatization’s product could be analyzed by MS in ESI mode which is superior to UV detection used in other methods. Furthermore, the accurate mass analysis of Q-tof facilitates the identification of unknown amino acids in Huangqi injection. The method provides good separation, reliable qualification and quantification of 19 amino acids in complex matrices.

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Tuesday 3:00 PM
Poster #68 in Exhibit Hall

**Meconium Targeted Drug Screening in 9 Seconds Per Sample Using Laser Diode Thermal Desorption Mass Spectrometry (LDTD-MS/MS)**

*Pierre Picard* - Phytronix Technologies (p.picard@phytronix.com)

- Drug abuse during pregnancy is a major medical issue associated with significant maternal and infant complications. Meconium is a common specimen used to identify drug-exposed infants. The proposed mechanism for drug presence in the meconium is that the fetus excretes the drug into bile and amniotic fluid. Current analysis method uses several immunoassays to cover many drugs. To reduce the number of screening reagents, required quantity of meconium and analysis time, a Laser Diode Thermal Desorption Mass Spectrometry (LDTD-MS/MS) method was developed. A fast extraction method is used with calibration range of: 20 to 200 ng/g for amphetamines/cocaine/opiate/oxycodone/PCP/methadone and 50 to 500 ng/g for Barbiturates/Benzodiazepines classes. The lower limit of the calibration curves represents the cutoff for reporting results. Sample analysis time is 9 seconds per sample.
Tuesday 5:00 PM
Poster #69 in Exhibit Hall

Characterizing Matrix Depletion Using a Novel 96-well Format Extraction Media - Tecan® AC Extraction Plate™ (AC Plate).

**Judy Stone** - Univ. of Calif. San Diego Health System (jastone@ucsd.edu)

- We interrogated the AC Plate to characterize serum phospholipid (PL) depletion. Extraction recovery, matrix effect, and chromatography were evaluated for testosterone, 13C3-testosterone, and eight PL MRMs. We compared the effects of varying pH, organic content (% methanol or acetonitrile) and two protein-binding releasing agents (ZnSO4 or LiCl/ammonium formate) in the AC Plate extraction reagent versus simple acetonitrile or ZnSO4/methanol protein precipitation with and without filtration through a Sigma HybridSPE® plate. The AC Plate reduces background PL by 4 orders of magnitude compared with simple acetonitrile precipitation while providing sufficient sensitivity to measure 1 ng/dL of testosterone in 100 uL of serum.

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Tuesday 3:00 PM
Poster #70 in Exhibit Hall

Simple Extraction of Antidepressants from Whole Blood for LC-MS/MS Analysis Using Coated Well Plates

**Dave van Staveren** - Tecan Schweiz AG (dave.vanstaveren@tecan.com)

- Antidepressants are widely prescribed medications for the treatment of depression and other mental illnesses. Although in general having good safety profiles, they still carry some risk of side effects and fatal intoxication due to suicidal/accidental overdose. Therefore, the analysis of antidepressant drugs in blood samples is important in clinical and forensic toxicology. This poster describes the determination of different classes of antidepressants in human whole blood employing a straightforward sample preparation procedure based on the AC Extraction Plate and subsequent LC-MS/MS analysis.

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Tuesday 5:00 PM
Poster #71 in Exhibit Hall

High-sensitivity, High-Throughput Quantitation of Catecholamines and Metabolites in Plasma by Automated WCX-SPE Coupled to LC/MS/MS for Clinical Research

**Ichiro Hirano** - Shimadzu Corporation (i_hirano@shimadzu.co.jp)

- Plasma levels of catecholamines and their metabolites, namely norepinephrine, epinephrine, dopamine, metanephrine and normetanephrine, are of significant relevance in clinical research in the field of endocrinology and disease screening. Fast, high-sensitivity analytical system is warranted. To this end, we developed an optimized method for simultaneous determination of these compounds using Shimadzu LCMS-8060, achieving complete chromatographic separation and low pg/mL LLOQ in plasma within 5 minute analysis time. Sample preparation was automated by Biotage Extrahera using WCX-SPE in 96-well format. Pre-validation study was performed, including demonstration of quantitative consistency with HPLC-based predicate device.

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Tuesday 3:00 PM
Poster #72 in Exhibit Hall

High-sensitivity, High-Throughput Quantitation of Catecholamines and Metabolites in Urine by LC/MS/MS for Clinical Research

**Atsuhiko Toyama** - MS Business Unit, Shimadzu Corporation (toyama@shimadzu.co.jp)

- In this study, we demonstrated the analytical performance of two LC/MS/MS methods that quantitated urinary catecholamines and their various metabolites for efficient clinical research. One method involved acid hydrolysis of urine samples followed by solid phase extraction to quantitate deconjugated norepinephrine (NE), epinephrine (E), dopamine (DA), metanephrine (MN) and normetanephrine (NMN). The other method was a dilute-and-shoot method to quantitate free MN, NMN, vanillylmandelic acid (VMA), homovanillic acid (HVA) and 5-hydroxyindolacetic acid (5-HIAA). Both methods had quantitative range to cover biologically relevant concentrations and analysis time of less than 5 minutes.
Tuesday 5:00 PM
Poster #73 in Exhibit Hall

**Determination of Etonogestrel in Blood Plasma by High Performance Liquid Chromatography - Mass Spectrometry**

*Irina Zolkina - Pirogov Russian National Research Medical University* (izolkina81@gmail.com) -- *Young Investigator Grantee*

- Purpose. Development and validation of methods for determining plasma concentrations of etonogestrel (3-keto desogestrel). The method used - HPLC/MS. Analytical equipment - liquid chromatograph and a mass spectrometer with a triple quadrupole. Chromatographic conditions: analytical column C18 (75*2.1 mm, 3.5 µm), flow rate 0.4 ml/min, eluting with a gradient system (acetonitrile :water). Detection mode is MRM. Sample preparation is a liquid-liquid extraction with diethyl ether was concentrated and redissolved in 50% acetonitrile. Results. The recovery rate is 77%. Calibration curve is linear in the range 40-4000 pg/ml. The LLOQ is 40 pg/ml and LOD is 20 pg/ml.

Conclusions. Etonogestrel - active substance in the composition of many last-generation oral contraceptives. The method developed by HPLC/MS is sensitive enough to determine the picogram of etonogestrel in human plasma.

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Tuesday 3:00 PM
Poster #74 in Exhibit Hall

**A Liquid Chromatography-tandem Mass Spectrometry Method for the Detection of Beta-carotene in Serum**

*Jessica Gifford - Calgary Laboratory Services* (Jessica.Gifford@cls.ab.ca) -- *Young Investigator Grantee*

- Beta carotene is a fat-soluble compound routinely measured in serum because of its physiological importance as a vitamin A precursor. Most analytical techniques measure beta-carotene by liquid chromatography coupled to a diode array detector. These analytical techniques, however, suffer from poor analyte specificity and accuracy, and an inadequate variety of commercial kits that are expensive. To address this, we have developed a liquid chromatography-electrospray ionization tandem mass spectrometry (LC-ESI-MS/MS) method that measures beta-carotene in serum; a matrix that contains other carotenoids including alpha-carotene and lycopene (isobars of beta-carotene) and a variety of lipophilic molecules.

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Tuesday 5:00 PM
Poster #75 in Exhibit Hall

**Exposure Biomarker Discovery for Toxic Phthalate Plasticizers Using Liquid Chromatography-High Resolution Mass Spectrometry and Metabolomics Approaches**

*Pao-Chi Liao - National Cheng Kung University* (liaopc@mail.ncku.edu.tw)

- Phthalates, including DINP, DPHP, and DINCH, are used as plasticizers and could cause undesired health impacts, such as endocrine disrupting effects. Workers and general population are exposed to them, so assessment of their exposure is a public health issue. Therefore, exposure biomarker discovery for toxic phthalates is of great interest in occupational and environmental health. We used HRMS with metabolomics approaches, signal mining algorithm with isotope tracing (SMAIT), MDF, and XCMS, to filter out meaningful metabolite signals from complex LC-HRMS data. They were further verified as markers of toxic phthalate exposure using animal models and tested in general population.

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Tuesday 3:00 PM
Poster #76 in Exhibit Hall

**Evaluation of Lab Developed Test for Simultaneous Determination of Sirolimus and Everolimus by Liquid Chromatography Tandem Mass Spectrometry**

*Seungman Park - GreenCross Laboratories* (freenuri78@gmail.com)

- We developed and validated lap developed test for simultaneous determination of sirolimus and everolimus using liquid chromatography tandem mass spectrometry (LC-MS/MS). The accuracy, limit of quantification, precision, linearity, and carry-over were evaluated. The accuracy, precision, and linearity were excellent. The limit of quantification and carry-over were acceptable. But, result of proficiency test was unacceptable. After calibrator change, the concentrations of PT materials were within acceptable range. Although the LC-MS/MS assay shows excellent analytical performance, attending PT program is helpful for harmonization with peer group.
Fast Determination of 17-Hydroxyprogesterone by LC-MS/MS for Diagnosis of Congenital Adrenal Hyperplasia

**Daniel Zhou** - Stanford Health Care (DaZhou@stanfordhealthcare.org)

- STAT 17-hydroxyprogesterone [17-OHP] is commonly ordered for confirmation of congenital adrenal hyperplasia [CAH] mostly in neonates and pediatric patients. Rapid test turnaround time [TAT] is critical, especially in life-threatening salt-wasting cases. Since conventional LC-MS/MS requires a time consuming manual sample preparation step, we investigated commercially available dispersive pipette extraction tips [DPX tips] to shorten the sample preparation time with the aim of building a STAT test to meet a clinical diagnostic need. Results indicate that DPX tips are effective for 17-OHP analysis, and may reduce sample preparation time by 75%. This rapid method is able to meet the STAT test requirement for CAH confirmation in children.

Qualitative Analysis for Multiple Drugs in Urine by Liquid Chromatography Time-Of-Flight Mass Spectrometry (LC-TOF/MS)

**Kathryn Smith** - ARUP Laboratories (kathryn.smith@aruplab.com)

- Liquid Chromatography Time of Flight Mass Spectrometry (LC-TOF/MS) allows for the high-throughput detection of multiple drugs and non-targeted analysis making it a good choice as a primary screening tool. LC-TOF/MS was utilized here as a broad-spectrum screen to determine the drug involvement in cases of accidental or intentional overdoses. This comprehensive test includes a simple dilute and shoot method identifying the presence of 111 specific pharmaceutical compounds, illicit drugs and their metabolites in a patient’s urine. The investigation of the utility of reference mass infusion to monitor individual sample ion suppression will also be discussed.

High Throughput Screening of Urine Marker Codes by Laser Ablation Electrospray Ionization Mass Spectrometry

**Callee Walsh** - Protea Biosciences (callee.walsh@proteabio.com)

- Laser ablation electrospray ionization mass spectrometry (LAESI-MS) is a technique for high throughput screening from complex liquid matrices. LAESI-MS was used in high throughput screening of urine containing polyethylene glycol markers, which are used in drug screening to assure urine identity. Detectability of polyethylene glycol markers in urine indicate utility for expected concentrations within patient samples. For high throughput screening, data acquisition time was 2.3 seconds per well and 13 minutes for 96-well plate, considerably increasing efficiency.

Phospholipids as Potential Biomarkers for Ovarian Cancer: Spatial Localization and Use in Diagnosis

**Luisa Doria** - Imperial College, London (m.doria13@imperial.ac.uk) -- *Young Investigator Grantee*

- Ovarian cancer is the fifth most common cancer among women, mainly due to the poor and vague prognosis and diagnosis. DESI-MS is an excellent technique to characterize different cancer types. It provides detailed spatial information within the sample, providing the opportunity to investigate tumour biology from an entirely new perspective with accurate biochemical information about each tissue type. Using DESI coupled to a TQ for diagnosis makes this technique quicker and less expensive. Furthermore, it opens the possibility to use DESI for targeted imaging and quantification.
Tuesday 3:00 PM
Poster #82 in Exhibit Hall

**Performance Evaluation of the Multiplex Assays for First-line Anti-tuberculosis Drugs in Dried Blood Spots Using UPLC-MS/MS**

**Kyunghoon Lee - Seoul National University Hospital (khlee59023@gmail.com)**

- We developed an UPLC-MS/MS method for simultaneously measuring blood concentrations of ethambutol, pyrazinamide, rifampicin, isoniazid in Dried Blood Spots (DBSs). Each DBS sample was analyzed on the UPLC system and the assay performance was evaluated. All drugs were clearly separated within 3 min. Within-run and Between-run precisions were 6.1%-11.3% and 12.2%-28.8%. Linearity was acceptable for each drug. Inter-assay calibration variability data on five consecutive days showed a linear and reproducible curve in the observed analytical ranges. Favorable correlations between drug concentrations in DBSs and sera were observed except for rifampicin and isoniazid.

Tuesday 5:00 PM
Poster #83 in Exhibit Hall

**Measurement of Kynurenine-to-tryptophan Ratio as a Biomarker for Urinary Tract Infection**

**Melanie Yarbrough - Washington University School of Medicine (myarbrough@path.wustl.edu) -- *Young Investigator Grantee***

- Tryptophan (Trp) catabolism yields kynurenine metabolites through the activity of indoleamine-2,3-dioxygenase (IDO). The ratio of the product kynurenine (Kyn) to the substrate Trp is used as a surrogate for biological IDO enzyme activity. IDO expression is locally induced during urinary tract infection (UTI) to suppress immunity and facilitate bacterial colonization. We developed a tandem mass spectrometry assay to measure Trp and Kyn in biological samples and compared Kyn/Trp ratios in urine samples of healthy controls to symptomatic patients with and without UTI. Kyn/Trp ratios were non-specifically increased in symptomatic patients versus healthy controls. No difference was seen between symptomatic patients with and without UTI, indicating that Kyn/Trp ratios may serve as a general indicator of a systemic inflammatory process.

Tuesday 3:00 PM
Poster #84 in Exhibit Hall

**Quantitation of 22 Long Chain Fatty Acids by GC-NCI-MS in Serum and Plasma**

**Erik Kish-Trier - ARUP Laboratories (erik.kishtrier@aruplab.com)**

- Long chain fatty acids (LCFAs) play diverse and critical biological roles. Here we present a GC-NCI-MS method for quantitation of 22 LCFAs (C12-C22) in serum/plasma, including the essential and conditionally essential polyunsaturated LCFAs. Hydrolysis was used to release bound LCFAs, which were extracted in hexane and derivatized to form pentafluorobenzyl esters. Our GC strategy gave baseline separation for most analytes, prior to being ionized by NCI and detected in SIM mode. This method offers several advantages upon published studies by using a single injection, additional internal standards, and backflush technology. Validation data and updated reference ranges are presented.

Tuesday 5:00 PM
Poster #85 in Exhibit Hall

**A Coupled Analysis of Low and High Abundance Isotopes Extending the Dynamic Range of an Assay for Methamphetamine in Meconium via LCMSMS**

**Melissa Goggin - MEDTOX Laboratories (goggim1@labcorp.com)**

- A one-hundred fold increase in the dynamic range of an assay measuring methamphetamine in meconium has been achieved by relying on the natural isotopic distribution of carbon-13. Transitions corresponding to the predominant methamphetamine isotope (12C10-methamphetamine) are utilized for the lower region of the assay (5-1000 ng/g). Transitions corresponding to 13C2, 12C8-methamphetamine are additionally monitored, effectively reducing the analyte signal based upon a 0.54% probability that any given molecule of methamphetamine will possess two 13C isotopes. By monitoring the uncommon isotope, quantitation is extended from a ULOQ of 1000 to 100,000 ng/g with acceptable peak shape, and consistent qualifier ratios throughout.
High-Throughput Preparation of Cellular FAMEs and Sterols for GC/MS Analysis
Kevin Williams - University of California, Los Angeles (kevinwilliamsphd@gmail.com)

In recent years, metabolomic and isotopic enrichment analysis has led to breakthroughs in a variety of fields of research including cancer biology, immunology, and aging/regenerative medicine. This research has necessitated the preparation and analysis of ever increasing numbers of samples. There are considerable challenges to preparing metabolomics samples, especially in the preparation of cellular lipid samples. Here we describe a high-throughput procedure for the preparation of cellular fatty acids and sterols that reduces costs, labor and preparation time while increasing sample consistency. The resulting FAMEs and Sterols can then be analyzed by GC/MS for quantification and isotopic enrichment analysis.

Successful Implementation of Immunosuppressant Drugs (ISDs) Monitoring Using Liquid Chromatography Mass Spectrometry (LC-MS/MS)
Xiaowei Fu - Children's Hospital Los Angeles (xfu@chla.usc.edu) -- *Young Investigator Grantee*

We hereby report our experience at Children's Hospital Los Angeles (CHLA) in implementing therapeutic monitoring of ISDs including Tacrolimus, CyclosporineA, Sirolimus and Everolimus using LC-MS/MS. A quantitative multiple reaction monitoring (MRM) analytical method was validated on a Thermo-PRELUDE-TSQ-QUANTIVA LC-MS/MS including accuracy, precision, analytical sensitivity, reportable range, and recovery. In summary, a very simple, fast, sensitive LC-MS/MS method was successfully implemented in three months, which, when compared to the previously used immunoassay method, resulted in better optimization of therapeutic drug levels, decreased sample volumes, and significant cost savings.

Exploring the Sources of Cross Contamination in 96-Well Sample Preparation Prior to LC-MS/MS Analysis
Paul Roberts - Biotage GB Limited (paul.roberts@biotage.com)

In all areas of analytical testing it is vital to ensure proper measures are in place to reduce or eliminate cross contamination between samples, which could result in false positive and/or false negative results. Sample carryover in the LC/MS system is usually monitored early in the method development process. However, one area often overlooked is sample preparation. This involves multiple aspects: pipetting, sample transfer, extraction, evaporation and mixing steps. This poster will discuss various stages of the sample preparation process to determine the potential for cross contamination and present approaches to minimize and or eliminate the effect.

Preliminary Results from the Slovenian Expanded Newborn Screening Pilot Study
Andraz Smon - Biochemistry graduate (andraz.smon@kdj.si) -- *Young Investigator Grantee*

Newborn screening programme in Slovenia currently includes only two diseases, phenylketonuria and congenital hypothyroidism. Last year a pilot study of expanded newborn screening for inborn errors of metabolism using tandem mass spectrometry (MS/MS) started. 10000 dried blood spots from newborns were analysed retrospectively. Newborns with highest elevations of measured analytes were immediately investigated and three newborns with inborn errors of metabolism were found (not counting hyperphenylalaninemia/phenylketonuria); one case of VLCAD, a case of 3-MCC deficiency and a case of GA1. Based on these results the cumulative incidence of inborn errors of metabolism (detected by MS/MS) is high in Slovenia. Follow-up tests on selected newborns to set the cut-off values for chosen disorders are ongoing.
Identification of Two Frequent Hemoglobin Variants in Korea by Liquid Chromatography – Tandem Mass Spectrometry

Seung Jun Lee - Seoul National University Hospital (sjlee0318@gmail.com)

‣ We developed an UPLC-MS/MS method to identify hemoglobin (Hb) G-Coushatta and Hb Yamagata, common Hb variants in Korea, among suspected specimens detected by conventional HbA1c analyzers. All Hb variant specimens and normal controls were tested in UPLC-MS/MS system after the treatment with endoproteinase Glu-C. Two peaks, 689.8 m/z [M+2H+] and 832.4 m/z [M+3H+] at 6.36 min, and one peak, 832.4 m/z [M+3H+] at 10.78 min, were found to distinguish Hb G-Coushatta and Hb Yamagata from other Hb variants and normal, respectively. And the zygosity for these variants was determined by the intensity of two peaks: 657.8 m/z and 460.2 m/z.

Catecholamine Analysis: Method Optimization to Improve Sensitivity and Reduce Limits of Quantitation Using LC-MS/MS

Lee Williams - Biotage GB Limited (lee.williams@biotage.com)

‣ Catecholamines are classic biomarkers for the detection of diseases like hypertension, pheochromocytoma and neuroblastoma. The main target analytes - epinephrine, norepinephrine and dopamine, are traditionally analyzed using liquid chromatography with electrochemical detection. This poster discusses the impact of optimization of various parts of the method development process to maximise the sensitivity of LC-MS/MS analysis. A highly sensitive LC/MS system, a Shimadzu Nexera UHPLC coupled to an AB SCIEX 5500 triple quadrupole MS was used for analysis. Method parameters: pre-cursor ion selection, MRM transitions, chromatography and solid phase extraction protocols were optimised for increased sensitivity, allowing quantitation down to 20 pg/mL.

Comparison of Sample Preparation Strategies for the Extraction of Methylmalonic Acid from Serum Prior to LC-MS/MS Analysis

Rhys Jones - Biotage GB Limited (rhys.jones@biotage.com)

‣ This poster summarises various sample preparation strategies for the extraction of methylmalonic acid from serum prior to LC-MS/MS analysis. A range of extraction techniques were evaluated: protein precipitation, phospholipid depletion, supported liquid extraction and solid phase extraction using both silica and polymer-based mixed-mode anion exchange chemistries. Analysis was performed using an ACQUITY IClass UPLC interfaced to a Xevo TQS triple quadrupole mass spectrometer via electrospray ionization operating in multiple reaction monitoring mode. Method performance was evaluated for evaporative effects, assay recovery and ion suppression effects using post column infusion experiments. Phospholipid removal was also determined. Full results will be presented.
Posters by Day: WEDNESDAY

Wednesday 3:00 PM
Poster #2 in Exhibit Hall
**A Reference Measurement System for Urine Albumin**

*Ashley Beasley Green - NIST (ashley.beasley@nist.gov)*

- Urinary excretion of albumin is a major diagnostic and prognostic marker of renal dysfunction and cardiovascular disease; therefore, accurate measurement of urine albumin is vital to clinical diagnosis. To address urine albumin measurement precision, we have developed the following components of the urine albumin reference measurement system: a multiplexed candidate reference measurement procedure that utilizes isotope dilution-mass spectrometry (ID-MS) and multiple reaction monitoring (MRM) to quantify urine albumin; a primary reference material to be used as a calibrator for higher-order urine albumin methods; and a secondary reference material to be used as a matrix-based quality control for commercially-available urine albumin assays.

Wednesday 5:00 PM
Poster #3 in Exhibit Hall

**Method Development of LC-MS Based Peptide Quantitation Assay to Differentiate Kininogen and Kallikrein Cleaved Kininogen**

*Gul Mustafa - Protea Biosciences, Inc. (gul.mustafa@proteabio.com)*

- The purpose of this study was to develop a robust LC-MS based peptide quantitation assay to differentiate kininogen (HK) and kallikrein cleaved kininogen in order to determine a 2HK cut-point in plasma of healthy volunteers from patients with disease. MRM on an ABSciex 5500 QTrap mass spectrometer was done on various types of plasma samples. The target candidate peptides (SSRIGE, SSRIGEIKE, KKIYPTVNCQPLGMISLMK, and SYYFDLTDGLS) and 3-5 product ions for each peptide were validated empirically for plasma kininogen. Ratio of AUC for each peptide between different sample types was calculated. The ratio of SSRIGE peptide against HMWK vs LMWK unique peptide SYYFDLTDGLS has a potential to be used in an assay to differentiate plasma of healthy volunteers from patients with disease.

Wednesday 5:00 PM
Poster #5 in Exhibit Hall

**Sex Steroid Hormone Stability: Gel versus Non-gel Tubes**

*Sophie Hepburn - Prince of Wales Hospital (shepburn.au@yahoo.com) -- *Young Investigator Grantee* *

- We examined the stability of four sex steroids in serum stored at 4°C for up to 5 days. Serum collected into gel and non-gel containing tubes was analysed by LC-MS/MS for testosterone, androstenedione, 17-hydroxyprogesterone (n=20); and estradiol (n=27). Differences in measurand concentration at day 0 and following storage (day 1 and day 5) were evaluated for statistical / clinical significance. Androstenedione concentrations in gel-containing tubes were reduced by an average of 14% by day 5 (p<0.001), determined to be clinically significant. In addition, estradiol and testosterone concentrations were significantly increased in plain serum tubes by day 1 (p<0.01).

Wednesday 3:00 PM
Poster #6 in Exhibit Hall

**Immunosuppressant (Tacrolimus/Cyclosporin A) Monitoring by LC-MS/MS Using Mitra Microsampling Devices**

*Michael Mbughuni - Mayo Clinic (mbughuni.michael@mayo.edu) -- *Young Investigator Grantee* *

- Tacrolimus and Cyclosporin A are immunosuppressants commonly prescribed for solid organ (cardiac, liver, renal) transplants. Therefore, therapeutic drug monitoring of these medications is important based on their narrow therapeutic range where suboptimal concentrations can lead to organ rejection and elevated concentrations can lead to toxicity. Since transplant patients need to take these medications for life, this study looked at the feasibility of measuring Tacrolimus and Cyclosporin A using a high-performance liquid chromatography tandem mass spectrometry assay using driedblood from a microsampling device (20 mcL) compared to a validated method using 200 mcL venous collected EDTA whole blood.
Wednesday 5:00 PM
Poster #7 in Exhibit Hall
**Cost Effective Dilute-and-shoot Approach for Determination of Illicit Drugs in Oral Fluids Using LC-MS/MS**

*Kavinda De Silva - MTL (kavindad@moleculartestinglabs.com)*

- Due to a recent increase in the demand of Oral Fluid analysis, many challenges have been set forth in developing robust cost effective assays for determination of illicit drugs. As an alternate matrix to traditional urine for monitoring drugs, oral fluids poses far more challenges due to stability, detection limits and sample clean up. A method was developed for cost effective, dilute and shoot assay with linear ranges of 1-300ng/mL for selective drugs with R2 > 0.99 was validated.

Wednesday 3:00 PM
Poster #8 in Exhibit Hall

**LC/MS Analysis of Monoclonal Antibody Structure Utilizing HALO® BioClass Fused-Core™ Particles; Multilevel Analysis for Proteins and Glycovariants**

*Edward Faden - MAC-MOD Analytical (efaden@mac-mod.com)*

- The structural characterization of monoclonal antibodies (mAbs) is a challenging and complex task. Efforts have been directed at optimizing high performance HALO® BioClass Fused-Core™ silica materials in order to improve the separations component of LC-MS analysis of proteins, mAbs, glycopeptides and released glycans. Recently improved superficially porous silica packing materials have been applied to HPLC / UHPLC characterization of biomolecules including glycosylation variants from mAbs. HALO BioClass Fused-Core™ materials show considerable utility for analysis of these highly complex molecules, using conditions that permit excellent separations and analysis via LC-MS. Alternatives to standard trifluoroacetic acid (TFA) and formic acid (FA) mobile phase conditions are shown for intact molecule separations, subunit analyses, and for analysis of tryptic digests.

Wednesday 5:00 PM
Poster #9 in Exhibit Hall

**Improving the Detection of Thyroglobulin in Human Plasma for Clinical Research by Combining SISCAPA Enrichment and Microflow LC/MS**

*Jay S. Johnson - Waters Corporation (jay_johnson@waters.com)*

- Use of an optimized SISCAPA enrichment that is highly specific for a signature peptide of thyroglobulin combined with microflow LC/MS using a vetted dual-pump trapping configuration provides a sub 1 ng/mL quantification limit of Tg protein with a cycle time of 6.75 min. This quantification limit is comparable with the best in literature for standard flow LC/MS. Microflow also offers other tangible benefits including the use of five times less starting plasma and half the injection volume of the standard flow method to reach this detection limit while being more precise. Accordingly, microflow is a viable and attractive solution for clinical research.

Wednesday 3:00 PM
Poster #10 in Exhibit Hall

**Improving Biochemical Content - Discriminating Lipid and Metabolite Distribution Using DESI and High Resolution Mass Spectrometry in Healthy and Diseased Tissue**

*Joseph Kennedy - Prosolia, Inc. (kennedy@prosolia.com)*

- The determination of the distribution of lipids and metabolites in tissue samples is of seminal importance to understanding disease and biochemistry. DESI imaging is important for its ability to provide objective molecular information in histological context without perturbing the integrity of the tissue. The majority of the experiments done using DESI have provided nominal mass information. Both lipids and small molecule metabolites have many nominal mass isobars including phosphatidylserines, cholines, and sulfatides which can differ by less than 50 mDa. Here the need for accurate mass (< 3 ppm), high mass resolution (> 40,000) information are demonstrated. Examples showing differential tissue distribution of isobaric metabolites and lipids differing by < 50 mDa are provided in a variety of tissues and the benefits to understanding disease and fundamental biochemistry are discussed.
Analysis of Urinary Free Catecholamines and Metanephrines by Tandem Mass Spectrometry: Validation and Implementation in a Clinical Laboratory

Anna Robson - Heart of England NHS Foundation Trust (anna.robson1@nhs.net) -- *Young Investigator Grantee*

- Analysis of both urinary free catecholamines and metanephrines are used in the diagnosis of phaeochromocytoma. This poster describes the development, validation and implementation of a new SPE-LC-MS/MS (solid phase extraction – liquid chromatography - tandem mass spectrometry) method for urinary free catecholamines and metanephrines. The poster also demonstrates the capability of this new method to incorporate both catecholamines and metanephrines in a single analysis.

All Roads Lead to Robots: Automation of Customized, Effective Trypsin Digestion

Qin Fu - Cedars Sinai Medical Center (qin.fu@cshs.org)

- Precise protein quantification is essential for both discovery and targeted protein workflows. It requires reproducible protein proteolysis that consistently generates the same peptide in each sample type. Here, we have developed a robotic MS samples preparation workflow by using a Biomek NXP workstation. The workflow is completely hands free with flexible denaturation and proteolysis time for sample specific conditions (e.g. plasma, urine, IPSC, and tissue). It improved reproducibility and throughput by approximately 4 and 7 fold compared to manual processing. We will present expanded automation workflows, to assist in quality control (QC), digestion optimization, and digestion reproducibility testing for large scale LC-MS based analysis.

A Workflow for Drug Discovery from Environmental Samples Using Molecular Networks

Stefano Bonissone - Digital Proteomics LLC (stefano@digitalproteomics.com)

- The problem of identifying non-reference encoded biomolecules using tandem mass spectrometry can be avoided by comparing spectral similarities and building a network based on these similarities. Nodes in such a network represent spectra, while edges connect similar spectra with small mass differences. The spectral network approach allows the identification of new molecules by creating a network containing labeled spectra. These labeled nodes allow the determination of similar molecules occurring as proximal nodes in the graph. We demonstrate this molecular network approach using an environmental sample, utilizing spectral libraries from known natural product compounds to find new, similar, candidates from the environment.

Toxicology Testing in Complex Patient Populations Requires Definitive Testing

Emily Ryan - LabSource, LLC (eryan@labsource.net)

- Our objective was to assess the differences in detection rates in a diverse population for the screen and confirm paradigm versus direct to definitive testing for urine toxicology testing. 4794 urine specimens were qualitatively screened for the presence 17 different drug or drug classes on the Olympus AU680 analyzer (Beckman Coulter, Inc., Brea, CA). All samples were then quantitatively tested on an LC-MS/MS platform (Sciex, Framingham, MA or Agilent Technologies, Santa Clara, CA) for the free and conjugated forms of 74 analytes. Data were reviewed to determine what positive specimens would have been missed if only screened positive results were reflexed for LC-MS/MS testing. With the current complexity of pharmaceuticals immunoassay testing missed a compound in 44% of the specimens. Mass spectrometry methods are essential to obtain an accurate results for treatment decisions.
Utilizing Western Blot and Mass Spectrometry to Improve Immunohistochemical Detection of Predictive Biomarkers in a Clinical Setting
Heather O’Neill - Caris Life Sciences (honeill@carisls.com)

Antibody specificity is a potential source of variability in immunohistochemical (IHC) clinical assays. To verify specificity for downstream IHC testing of TLE3 protein, anti-TLE3 antibodies from three separate vendors were analyzed by western blot and subsequent mass spectrometry of gel-excised bands to confirm target specificity. All three anti-TLE antibodies identified a common ~83 kD band by western blot, in addition to several bands of differential molecular weights. High-resolution mass spectrometry was used to verify specific target bands and identify which antibodies resulted in detection of non-specific targets. The results demonstrate the utility of western blot combined with mass spectrometry as a supplemental quality control for IHC testing.

Differential Recovery of Gabapentin and Pregabalin Utilizing SPE Extraction Demonstrated in a 42 Analyte Urine Confirmatory LC-MS/MS Panel
Karsten Liegmann - California State Polytechnic University, Pomona (karsten.liegmann@speware.com)

Methods that quantify a wide variety of drug chemistries from a single analysis are increasingly being implemented. An impediment to implementation of these methods is inclusion of gabapentin and pregabalin to these comprehensive methods, as specimens routinely have concentrations in the hundreds of microgram per milliliter range. The concentration and types of organic solvents used in the elution step can be modified to predictably and reproducibly reduce the recovery of gabapentin and pregabalin, while not affecting the complete recovery of analytes requiring high levels of sensitivity.

Sensitive Measurement of Plasma 1,25-Dihydroxyvitamin D2&3 (125DHVD) via LC-MS/MS: A Simple SPE Sample Preparation and MS Sensitizing Derivatization Process
Qi Huang - Quantalytical Labs (qi.huang@speware.com)

The physiologically active forms of Vitamin D, 1,25-dihydroxyvitamin D2/3 (DHVD) are important biomarkers for a number of disease states. With recent advancements in LC-MS/MS technology, reliable measurements of DHVD are still challenging due to low abundance and poor ionization capacity, even with the aid of PTAD, a Cookson type derivatization reagent. There were reports of quantification of DHVD with a combination of immuno-affinitive capture and PTAD derivatization. In this presentation, we will report quantification of plasma DHVD with a simple SPE and quick derivatization with an in house developed novel crown-ether based PTAD reagent.

Unified Drug Testing by Online SPE-LC/MS/MS for High Productivity & Ease of Use: One Totally Automated Method Measures ALL Drugs in Urine & Oral Fluids
Mark Hayward - ITSP Solutions (Mark.Hayward@ITSPsolutions.com)

Continued growth of LC/MS/MS for drugs of abuse in urine and OF seems certain. However, there are technical challenges that need to be met. These include easily measuring low dose drugs at or near 1 ng/g concentration (medical purposes, Pesce, 2012 AACC conf,& zero tolerance testing), simplicity performing measurements with lab technicians, and ability to achieve high productivity for all work while minimizing the labor and number of workflows required. To meet these needs, we have developed an automated on-line SPE-LC/MS/MS method. It uses SPE to clean / pre-concentrate samples so that low dose drugs at or near 1 ng/g concentration are easily measured at S/N ≥20. At the same time, the method’s design is balanced to address all of the drugs (acidic/basic drugs & polar / non-polar drugs), as well as urine and/or OF samples, all in one method, all in one workflow.
Use of a Novel C18-Based Stationary Phase for Human Urine Metabolite Profiling by UHPLC-High Resolution Accurate Mass Spectrometry (HRAM)

Alan McKeown - Advanced Chromatography Technologies Ltd (amckeown@ace-hplc.com)

Profiling urine can provide useful information to aid clinical diagnosis. The use of UHPLC and High Resolution Accurate Mass (HRAM) instrumentation in clinical laboratories has grown considerably in recent times. Here, a novel C18 based polar embedded column (ACE Excel 1.7um C18-Amide) is used. This unique stationary phase has been designed to retain and separate a range of polar and non-polar species. Using an 8 minute broad gradient with HRAM it was possible to demonstrate the profiling capability of the method for a wide range of naturally occurring small polar molecules in urine.

Ultra Performance Liquid Chromatography-Tandem Mass Spectrometry Determination of Tryptophan and Its Kynurenine Metabolites

Li Wang - BC Children's Hospital (li.wang@cw.bc.ca) -- *Young Investigator Grantee*

Maternal tryptophan and kynurenine pathway metabolites have been found to be associated with the risk of pre-eclampsia. In order to explore the role of these metabolites in predicting pre-eclampsia, we aimed to establish a simple and rapid ultra performance liquid chromatography-tandem mass spectrometry (UPLC-MS/MS) method to measure tryptophan, kynurenine, and kynurenic acid in both plasma and urine samples. Samples/deuterated internal standards were deproteinized with methanol and injected without derivatization (Acquity Xevo TQ MS, Waters Corporation). Validation of the method was based on Clinical and Laboratory Standards Institute protocol C62-A (Liquid Chromatography-Mass Spectrometry Methods).

Change in Redox Balance Couples with Redistribution of Metabolic Flux to Protect Glutathione-deficient Gclm-knockout Mice from Alcoholic Liver Disease

Soumen Kanti Manna - Saha Institute of Nuclear Physics (soumen.manna@saha.ac.in)

Alcoholic liver disease (ALD) is known to progress via steatosis. Although factors contributing to the outcome are not fully understood, oxidative stress is known to be involved. Our recent study showed that glutathione-deficient (Gdm-null) mice, surprisingly, protected from alcoholic steatosis compared to wild-type mice. In order to investigate the mechanism, the reorganization of the polar metabolome was examined using HILIC-ESI-MS. The analysis revealed that shift in redox balance due to glutathione depletion takes place in tandem with redistribution of acetyl CoA flux into alternative metabolic pathways. This siphons alcohol-derived acetyl CoA away from de novo lipid biosynthesis leading to the observed protection of Gclm-null mice from alcoholic steatosis.

Tackling the Interference Problem for Estradiol Analysis by LC-MS/MS, Using Differential Ion Mobility Spectrometry

Michael J. Y. Jarvis - Sciex (michael.jarvis@sciex.com)

The measurement of low pg/mL concentrations of estradiol in serum and plasma, by LC-MS/MS, requires a highly sensitive method. To be sure, the sensitivity challenge is significant. Nevertheless this requirement can be readily addressed with the use of high performance tandem mass spectrometry instrumentation, larger sample volumes, and extensive sample preparation. However, those familiar with this analysis will be acutely aware of the more urgent selectivity challenge posed by the presence of ubiquitous, low-level, non-specific chromatographic interferences that frequently mask the presence of the target estradiol peak. In the work presented here, differential ion mobility spectrometry (DMS) has been employed to enhance the selectivity of the analysis, while enabling the measurement of <1 pg/mL estradiol in serum, using a simple one-step liquid liquid extraction sample preparation.
A Validated Amino Acid Analysis Assay for Accurate Quantification of Stable Isotope Labeled Thyroglobulin and Other Protein Reference Materials

Kevin Ray - MilliporeSigma (kevin.ray@sial.com)

With the emergence of mass spectrometry for the clinical measurement of proteins in biological matrices, the development of biological reference materials will continue to grow in importance. Certified Reference Materials with values assigned by metrologically valid procedures will be critical to minimize and control experimental variations in all steps of the workflow including protein extraction, fractionation, enrichment, proteolysis and analysis. To this end, we have verified sequence fidelity and isotopic incorporation of an SIL full length Thyroglobulin for use as an internal standard in quantitative MS workflows. We have also developed an amino acid analysis (AAA) method traceable to NIST SRM 2389 and validated the method against NIST SRM 927. This AAA method may be used for accurate quantification of proteins to enable development of accuracy-based protein reference materials.

Use of an Animal-free Synthetic Surrogate Serum Matrix for Assay Calibrators, Controls, and Patient Sample Diluent in ELISA and LC-MS Based Clinical Assays

Jim Walters - MilliporeSigma (jim.walters@sial.com)

The objective is to determine the utility of a well-defined, stable, animal-free matrix for use as a serum (or stripped serum) substitute in clinical assays. The synthetic surrogate matrix was prepared with 2% rHSA expressed from rice. It was tested in commercially available IVD ELISA kits with two different analytes (β-2 microglobulin and thyroglobulin), and in direct comparison to human serum in LC-MS based clinical assays for methotrexate, testosterone and estradiol in blood. For all comparative analyses the synthetic surrogate serum matched the performance of the matrix provided by the kit manufacturers, pooled human serum and stripped human serum with no interferences observed and with correlations of R² > 0.998. We have formulated a simple, animal-free, analyte-free matrix which has been shown to be suitable as a calibrator/blank matrix as well as a patient sample diluent.

Generic Sample Preparation Methodology for the Analysis of Steroid Hormones by LC-MS/MS for Clinical Research

Dominic Foley - Waters Corporation (dominic_foley@waters.com)

Care must be taken when developing steroid hormone analytical methods for clinical research, to limit interferences which affect accuracy and precision. MS/MS provides a way to selectively differentiate between these hormones, while chromatography can provide separation of isobaric species. However, sample preparation is the key in providing LC-MS/MS analytical sensitivity by reducing matrix effects. We have developed an LC-MS/MS approach for the analysis of a wide range of steroid hormones. Extraction analytical sensitivity and phospholipid removal capability have been explored, which has shown that for a generic approach to steroid analysis, Oasis® PRIME HLB SPE is the most favourable option in providing optimal LC-MS/MS sensitivity. For Research Use Only, Not for Use in Diagnostic Procedures.

Application of Microfluidic Tandem Quadrupole LC-MRM-MS Based Translational Research Analysis of Putative Heart Failure Peptide Biomarkers in Human Plasma

Khalid Khan - Waters Corporation (Khalid_Khan@waters.com)

The application of tandem quadrupole mass spectrometry with integrated microfluidic chromatography (IonKey) for the analysis of proteolytic peptides in human plasma is described. A tandem quadrupole platform was used for its performance in terms of sensitivity, precision, and linearity and IonKey was selected due to its balance of sensitivity and throughput. This LC-MS configuration was utilized to demonstrate that proteolytically digested, non-depleted plasma samples from heart failure patients could be classified with good discriminative power using a subset of proteins previously suggested as candidate biomarkers for cardiovascular disease.
 Discrimination of Diabetic Lipid and Metabolite Profiles in Plasma in the Zucker Rat Model Using PaperSpray-High Resolution Mass Spectrometry

Justin Wiseman - Prosolia (wiseman@prosolia.com)

- The relative distribution of metabolites and lipids in serum has been linked to a broad range of disease states, among them diabetes. The analysis of the samples typically requires various levels of sample preparation followed by time-consuming and costly analysis using HPLC-MS. A simple and informative screen could provide rapid information to make differential health determinations is discussed here. Serum samples from diabetic, fatty and control rats is analyzed using paper spray interfaced to high resolution mass spectrometry. The analysis is simple and uses positive and negative ion modes. For a small sample set (n=3 each for control, fatty and diabetic Zucker rats) significant differences in phosphatidyl and lysophosphatidyl cholines, ethanolamines, serines and other lipids, and in small molecule metabolites including fatty acids. The 2 minute analysis uses 15 mcl of sample.

Hydrolyze Your Way to Compliance – a Call for Pain Management Certified Reference Materials

Heather Hochrein - UC San Diego Health System (hhochrein@ucsd.edu)

- There are many published studies on the performance of commercially available beta-glucuronidases obtained from different sources used for the hydrolysis of glucuronide-conjugated opioids. We have applied several studies testing three enzymes (beta-glucuronidase from Helix pomatia from Sigma-Aldrich, beta-glucuronidase from Haliotis rufescens from Kura Biotec, and a recombinant beta-glucuronidase from IMCS) for hydrolysis efficiency using spiked standards of parent drug and their corresponding glucuronides. We also performed a selected patient comparison focused on the glucuronide-species of interest, concentrating on parameters that could influence interpretation of results in a clinical setting. We saw up to 12-fold differences in recovery for total codeine, hydromorphone, morphine, and oxymorphone.

A Multi-Class Drug and Metabolite Screen of 231 Analytes by LC-MS/MS

Shane Stevens - Restek Corporation (shane.stevens@restek.com)

- Therapeutic drug monitoring can be challenging due to the low cut-off levels, potential matrix interferences and isobaric drug compounds. To address these challenges, many drug testing facilities are turning to liquid chromatography coupled with mass spectrometry (LC-MS/MS) for its increased speed, sensitivity, and specificity. The Raptor™ Biphenyl column was developed to complement high-throughput LC-MS/MS analyses by combining the increased efficiency of superficially porous particles with the resolution of Ultra Selective Liquid Chromatography™ column technology. In this example, a method was developed for a 231 compound multi-class drug and metabolite screen.

Rapid Evaporative Ionisation Mass Spectrometry (REIMS) as a Novel Approach to Microbial Community Profiling

Adam Burke - Imperial College, London (a.burke@imperial.ac.uk) -- *Young Investigator Grantee*

- Mass spectrometric methods are already integrated into diagnostic workflows of clinical microbiology laboratories; hastening and simplifying the turnaround for sample specimens and therefore leading to better patient outcomes. However, current commercial systems rely on isolating and culturing target microorganisms, followed by further sample preparation for MALDI-ToF, leaving room for further improvement. Rapid evaporative ionisation mass spectrometry (REIMS) has been shown to offer robust species identification for a range of clinically important microorganisms. Taxonomic markers have been identified in mixed cultures, demonstrating potential for taxonomic classification in non-pure samples. Work is currently underway to develop and optimise the application of the REIMS technology directly from samples, removing the need to first isolate and culture the microorganism of interest.
Wednesday 5:00 PM
Poster #39 in Exhibit Hall
**Preserving Specimen Integrity in Plasma Renin Activity Measurements**
*William O. Slade - LabCorp (Sladew@labcorp.com)*

- Plasma Renin Activity (PRA) measures the capacity of circulating Renin and Angiotensinogen to generate Angiotensin 2 (Ang2) using the quantity of its precursor, Angiotensin 1 (Ang1), which is linearly correlated with Ang2 abundance and, thus, predicts hypertension (1,2). Historically, EDTA plasma is the required specimen type for measurement of renin activity due to the chelation of divalent cations from the plasma, which reduces degradative loss of Ang1 to Ang2 during the "generation" procedure by conversion from the metalloprotease, Angiotensin Converting Enzyme (3). As a reference laboratory that receives many incorrect specimen types, we tested the stabilizing effect of supplemental EDTA on Ang1 in EDTA and non-EDTA samples types. Our preliminary results indicate that supplemental EDTA is required to prevent degradation of Ang1 regardless of sample type.

Wednesday 3:00 PM
Poster #40 in Exhibit Hall
**LC-MS/MS Method Development Challenges for the Separation of Non-Steroidal Anti-Inflammatory Drugs (NSAIDs)**
*Frances Carroll - Restek Corporation (frances.carroll@restek.com)*

- Nonsteroidal anti-inflammatory drugs (NSAIDs) are the most common medications worldwide for the treatment of pain, fever, and inflammation. Although NSAIDs are generally considered safe, long-term use can result in renal failure or serious gastrointestinal and cardiovascular side effects. Monitoring their use can help prevent drug interactions and to minimize side effects. For this analysis, the combination of the Raptor™ Biphenyl column, use of scheduled polarity switching, and selection of mobile phases that maximized sensitivity in both positive and negative ion modes allowed the simultaneous detection of 27 NSAIDs (plus acetaminophen) in one fast 8.5 minute analysis.

Wednesday 5:00 PM
Poster #41 in Exhibit Hall
**Accurate and Precise Sample Introduction at the Micro-Level: A New Approach to Routine, High Throughput Analysis for Trace Element Quantification with ICP-MS**
*Peter Winship - Teledyne CETAC Technologies (pete.winship@teledyne.com)*

- Particularly in clinical analysis, there is a growing demand for routine trace element quantification from samples of a very low volume. By pairing an advanced automation platform with an appropriate nebulizer/spray chamber it is now simple to reproducibly introduce liquid samples from the low microlitre level (< 5 µL) into the milliliter level to an inductively coupled plasma mass spectrometer (ICP-MS). Such sample introduction technology allows the analyst to work with greater confidence with precious samples and limited volumes with reduced or no compromise as to the analyte suite of interest and the number of replicate measurements. We report on the application of this technology to sample handling/introduction and measurement of trace element analytes, notably platinum, in human blood serum – a routine test in toxicology studies associated with platinum based chemotherapies.

Wednesday 3:00 PM
Poster #42 in Exhibit Hall
**Development and Validation of a LC-ESI-MS/MS Quantification Method of 25-hydroxyvitamin D2&D3 and of their C3-epimer**
*Pierre-Luc Mallet - University of Montreal, CIUSSS-CHUS (Pierre-Luc.Mallet@USherbrooke.ca) -- *Young Investigator Grantee*

- Development and validation of a LC-ESI-MS/MS quantification method of 25-hydroxyvitamin D2&D3 and of their C3-epimer (25-OH-D) has been performed to overcome the issue with the overestimation of vitamin D levels caused by the occurrence of C3-epimers. Briefly, samples were deproteinized using ZnSO4 and MeOH, extracted using heptane, dried down, and finally solubilized in the mobile phase (MeOH 68 %/ formic acid 0.1 %). Liquid chromatography was performed using isocratic gradient with a pentafluorophenyl column. CV and Bias were respectively inferior to 20 % and to 15 % for 3 nM of 25-OH-D. Method comparison was performed with another lab using an LC-ESI-MS/MS technique and we have obtained a slope and intercept of respectively 0.998 and 0.05 nM for total 25-OH-D. This LC-ESI-MS/MS method allows quantification of 25-OH-D2&D3 and of both C3-25-OH-D2&D3 which a few labs offer.
Wednesday 5:00 PM  
Poster #43 in Exhibit Hall  
**Quantitative Imaging of Platinum Based on Laser Ablation-inductively Coupled Plasma-mass Spectrometry to Investigate Toxic Side Effects of Cisplatin**  
*Tom Weaver* - Teledyne CETAC Technologies (tomas.weaver@teledyne.com)  
• This work presents a quantitative bioimaging method for platinum based on laser ablation-inductively coupled plasma-mass spectrometry and its application for a biomedical study concerning toxic side effects of cisplatin. To trace the histopathology back to cisplatin, platinum was localized and quantified in major functional units of testicle, cochlea, kidney, nerve and brain sections from cisplatin treated mice. The direct consideration of the histology enables precise interpretation of the Pt images and the novel quantitative evaluation approach allows significantly more precise investigations than the pure image.

Wednesday 3:00 PM  
Poster #44 in Exhibit Hall  
**Detection and Direct Quantitation of Guanidinoacetate, Creatine and Creatinine in Human Urine by LC-MS/MS and Electrospray Ionization**  
*Thomas Lynn* - Quest Diagnostics, Inc. - Nichols Institute (thomas.c.lynn@questdiagnostics.com)  
• The cerebral creatine deficiency syndromes (CCDS), inborn errors of creatine metabolism, include the two creatine biosynthesis disorders GAMT deficiency and AGAT deficiency), and the X-linked creatine transporter [SLC6A8] deficiency. Specimens were prepared by diluting urine with ultrapure water. A minimum sample volume of 100 µL was used. The diluted sample mix was injected onto an Agilent 1200 Series HPLC system using a reverse-phase column. Analysis was performed by positive electrospray ionization using an Agilent 6410 triple quadrupole mass spectrometer. Measurements of these three analytes in urine allow for the biochemical diagnosis of CCDS. The ability to measure all three analytes directly in the urine, with a very simple method of sample preparation, offers advantages over previous methods involving derivatization and indirect calculations.

Wednesday 5:00 PM  
Poster #45 in Exhibit Hall  
**Automated, High Throughput Quantitative Analysis of 39 Drugs of Abuse in Oral Fluid Using DPX Extraction and LC-MS/MS**  
*William Brewer* - DPX Labs, LLC (bill.brewer@dpxlabs.com)  
• A high throughput sample preparation method for drugs of abuse (39 compounds) in oral fluid was developed using DPX tip technology coupled with the Hamilton NIMBUS96 robotics system. A well plate of 96 samples takes 10 minutes to complete sample preparation followed by solvent evaporation, reconstitution and injection into the LC-MS/MS system. The method was evaluated for linearity, precision, extraction efficiency, and limits of detection and quantitation. The method established herein is highly reproducible and provides the necessary sensitivity for forensic and clinical purposes.

Wednesday 3:00 PM  
Poster #46 in Exhibit Hall  
**Enhanced Recovery of Trypsin Digested Proteins Using Dispersive Pipette Extraction for Downstream Proteomic Analysis**  
*Yuzhe Nie* - University of South Carolina (nieyuzhe@gmail.com)  
• For clinical proteomics, targeted peptides/proteins extraction and desalting efficiency are essential to obtaining high quality mass spectra data. In this study, we report a novel peptide purification method using IMCStips™, a disposable pipette extraction tip with sorbent loosely contained inside a pipette tip. Using human serum albumin as a model protein, the trypsin digested samples were readily purified using IMCStips™ packaged with reverse phase resin. The purification improved MS peak intensities, S/N ratios and sequence coverage significantly in comparison to other commercially available tips. Similar results have been obtained with other proteins, like human prealbumin, ß2-glycoprotein and transferrin. Since this method can be used in an automated online format, we envision it to be applied in the clinical proteomics studies, especially for low abundance peptides.
**The Role of Specimen Handling Time on the Interpretation of Plasma Acylcarnitine Profiles for the Diagnosis of Inborn Errors of Fatty Acid Metabolism**

*Tiffany Thomas* - Columbia University Medical Center (tt2254@cumc.columbia.edu)

- Analysis of plasma acylcarnitine profiles plays an important role in the diagnosis and management of patients with inborn errors of fatty acid metabolism. A pattern of elevated long-chain acylcarnitines (C16 to C18:2-carnitine) is associated with impaired carnitine cycle function as well as defective long-chain fatty acid metabolism. Blood collected from 3 subjects was immediately processed (spun, plasma separated, frozen) or left at room temperature for 2, 4, 6, 8, 24, or 48 hours and subsequently processed and analyzed by FI-ESI-MS/MS. Specimens left unprocessed for greater than 8 hours were associated with elevated C16 to C18:2-carnitine in all three subjects. No elevation of long-chain acylcarnitines was observed in plasma left at room temperature. Careful control of pre-analytical handling time is imperative for the correct interpretation of plasma acylcarnitine profiles.

**Development and Validation of PreTRM™ - A Multi-Protein Predictor of Spontaneous Preterm Birth**

*Chad Bradford* - Sera Prognostics, Inc. (cbradford@seraprognostics.com)

- Spontaneous preterm delivery, the leading cause of mortality and morbidity in neonates, lacks an adequately performing diagnostic test. Targeted quantitative proteomics approaches allow for interrogating multiple biological pathways in a single assay. 5,501 pregnant women were enrolled in the Proteomic Assessment of Preterm Risk (PAPR) clinical trial. Utilizing subsets of PAPR serum samples and several QC pools, the performance of 147 candidate proteins was determined in development and verification studies. Using two proteins with acceptable performance, a PreTRM™ score for spontaneous preterm delivery risk was validated.

**Heat Stabilization Preserves the Molecular Integrity of the Sample**

*Ylva Elias* - Denator AB (ylva.elias@denator.com)

- Active enzymes rapidly change the composition of biomolecules after sampling. Subsequent analytical results reflect a mix of the in vivo status and degradation products with increased inter-sample variation. The proteome, metabolites, and existing or potential biomarkers are affected. We describe efficient enzyme inactivation and standardization of sample handling using a heat-stabilization technology to eliminate degradation. Comparisons were made to standard snap-freezing and inhibitors. The results show that heat inactivated samples reflect the in vivo status as closely as possible which enables analyses to differentiate true biomarkers from those degradation products found in any situation where cells are under stress.

**A New Instrument that Combines Fast Microfluidic Separations with High Pressure Mass Spectrometry for Clinical Diagnostic Applications**

*Christopher Brown* - 908 Devices (cbrown@908devices.com)

- We have developed a prototype instrument that combines microfluidic capillary electrophoresis (CE) with high pressure mass spectrometry (HPMS) into a single benchtop instrument. This instrument is roughly the size of a conventional HPLC pump, and it contains all of the components necessary for running microchip CE-ESI-HPMS, including a small, custom-built scroll pump, and an on-board computer. We have used this platform to generate some preliminary data for applications relevant to clinical diagnostics including simulations of newborn screening via dried blood spot analysis and monitoring of pain management drugs in urine. This presentation will provide an overview of the instrumentation and examples of the data generated by this system.
Wednesday 3:00 PM  
Poster #52 in Exhibit Hall  
**A Total and Free Testosterone Method that Utilizes Automation and a Novel Microdialysis Plate to Achieve Efficient Workflow in a Clinical Laboratory**  
*Jennifer Fahse* - *Mayo Clinic* (fahse.jennifer@mayo.edu)  
Isotope dilution equilibrium dialysis (IDED) has long been considered the gold-standard method for free testosterone measurement. However, IDED requires a high sample volume and is labor intensive, making it a challenge for clinical laboratories processing hundreds of samples daily. We combined two necessary components of comprehensive testosterone testing, the measurement of the total testosterone concentration by LC-MS/MS and free testosterone by isotope dilution equilibrium dialysis, into a single automated method with the use of a microdialysis plate and robotic liquid handler.

Wednesday 5:00 PM  
Poster #53 in Exhibit Hall  
**Ion Mobility Mass Spectrometry: Alternative Drift Gas Selection for Improved Separation of Isomers in Clinical Analysis**  
*Christopher Chouinard* - *University of Florida* (chouinard@chem.ufl.edu) -- *Young Investigator Grantee*  
Ion mobility spectrometry (IMS) has been coupled with mass spectrometry to improve isomer separation capabilities without sacrificing time. To improve this potential, several strategies have been employed, including varying the drift gas environment. Although helium and nitrogen have been the traditional options, other drift gases have shown promise in improving resolution between isomers. This study will compare the most common drift gases, helium and nitrogen, to gases such as carbon dioxide, sulfur hexafluoride, and argon for their individual merits in improving separation of targeted clinical compounds, especially for Vitamin D metabolite epimers and steroid diastereomers such as testosterone and dehydroepiandrosterone.

Wednesday 3:00 PM  
Poster #54 in Exhibit Hall  
**Enzyme Hydrolysis of Haloperidol Glucuronide; a Major Urine Metabolite of Haldol®**  
*Gregory McIntire* - *Ameritox, LTD* (Greg.McIntire@ameritox.com)  
Haloperidol (Haldol®) is a typical antipsychotic prescribed for the treatment of acute symptoms of schizophrenia. Adherence to haloperidol therapy is monitored by evaluating levels of haloperidol and one or more metabolites reported to be present in urine at approximately 2 and 4% of the total dose. Unchanged Haldol® has been reported to be present in urine at less than 1% of the administered dose with no evidence of glucuronidation of the parent drug (Baselt, 10th ed). This work demonstrates that the parent drug is excreted in urine as the glucuronide and that hydrolysis can yield much higher levels of parent drug upon LC/MSMS analysis than observed upon direct injection.

Wednesday 5:00 PM  
Poster #55 in Exhibit Hall  
**Development of a Digested Yeast Protein Extract as a Mass Spectrometry Reference Material**  
*Candice Johnson* - *National Institute for Standards and Technology* (candice.johnson@nist.gov)  
The emergence of mass spectrometry (MS) based proteomic platforms utilized in biochemical and biomedical research has increased the need for high quality MS measurements. In an attempt to standardize MS metrics for the proteomics community, Saccharomyces cerevisiae yeast protein extract has been used in several successful inter-laboratory studies that demonstrated the yeast proteome as a suitable proteomic reference material (RM). To further improve on MS performance materials, we are developing a tryptic digest of yeast protein extract (RM 8313: Digested Yeast Protein Extract) to function as a quality control material to benchmark the performance of MS-based instrumentation. RM 8313 will facilitate the intra- and inter-laboratory assessment of MS-based instrument performance and measurement quality by eliminating the variability in laboratory protein digestion protocols.
Fat Soluble Vitamin Detection in Human Serum and Plasma by LC-MS/MS Using Biotage ISOLUTE SLE+ 96-well Plate Extraction

Jianqing (Ben) Lu - Prince of Wales Hospital (Ben.Lu@sesiahs.health.nsw.gov.au) -- *Young Investigator Grantee*

Traditionally HPLC methods have been used to analyse serum vitamins A, E and K, which involves extensive sample clean-up and long chromatographic run times. The aim of this study was to develop a single LC-MS/MS method for the determination of these fat soluble vitamins. Relatively low serum concentrations, the lack of availability of some authentic standards and occurrence of interfering lipids provided significant hurdles to method development. Here we present a simple and rapid method for the extraction and analysis of fat soluble vitamins in human serum and plasma, and the investigation of possibilities offered by MRM3 transitions for improved selectivity and sensitivity either as a front-line test or as a confirmation method.

Diagnostic Protein Quantitation of 26 Actionable Targets in Patient Biopsies Using Clinical Mass Spectrometry

Wei-Li Liao - NantOmics, LLC (Wei-Li.Liao@nantomics.com)

Many available oncology therapies target specific proteins. Additionally, protein biomarkers affecting chemotherapy efficacy have been identified. For targeted therapies to have maximal efficacy, it is necessary to identify patients whose tumors express the target protein. In this study we present a multiplexed Liquid Tissue-Selected Reaction Monitoring assay to simultaneously quantify 26 clinically-actionable proteins from a single microgram of FFPE patient tissue. The assay’s performance and tumor expression levels of these biomarkers in over 300 clinical biopsies will be presented. By providing absolute quantitation of multiple actionable proteins from patient biopsies, clinical mass spectrometry is delivering personalized cancer care.


Marta Kozak - ThermoFisher Scientific (marta.kozak@thermofisher.com)

The novel sample preparation method using solid phase micro extraction (SPME) blades was evaluated for analysis of 20 chemically diverse drugs of abuse in urine and plasma samples. Analytes were detected on a hybrid quadrupole-Orbitrap-based mass spectrometer. Urine and plasma samples were spiked with internal standards then diluted with buffer and water, respectively. The sample preparation method consisted of 4 steps which included: SPME blades conditioning, analytes extraction, wash step and elution step. Method was evaluated for limits of quantitation, precision and matrix effects. Limits of quantitation were in range of 0.1 - 5 ng/mL and method precision was better than 15% in both urine and plasma. Matrix effects in urine samples were compounds dependent and were in the range of 27.1-100 % recovery. Negligible matrix effects in plasma were observed: 79.0-119 % recovery.


Jia Wang - Thermo Fisher Scientific (jia.wang@thermofisher.com)

The research by Flow Injection Tandem Mass Spectrometry provides large quantities of information. The main advantage include no-chromatographic separation, rapid analysis time, low solvent consumption, and identification and quantitation of a large number of target analytes using their unique selected reaction monitoring transitions from precursor ions to product ions. We evaluated a meta-calculation software for automatic data processing. A total of 18 acylcarnitines and 12 amino acids were evaluated for each sample. Among 280 samples evaluated, a total of 8400 calculations of concentrations were processed. The manual transcription errors were eliminated, and processing time was improved from hours to minutes. For research use only. Not for use in diagnostic procedures.
Wednesday 5:00 PM
Poster #61 in Exhibit Hall
**Analyte or Amalgamation? Exploring Relationships and Redundancy in Metabolomic Datasets**
*Nathaniel Mahieu - Washington University* (nathaniel.mahieu@wustl.edu)

- Features in a metabolomic dataset are highly redundant. Annotation of these relationships and redundancies is key to data reduction, lower statistical significance thresholds, and a better understanding of metabolomic results. This poster presents an overview of: the types of relationships to be annotated in these datasets; poor assumptions of current annotation approaches and their corresponding failures; the computational challenge of this search problem; and a tool to explore these relationships. Of interest are how background ions contribute detected features, how peaks which have poor EIC correlation can still be related, and additional relationships which should be considered within these datasets.

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Wednesday 3:00 PM
Poster #62 in Exhibit Hall
**Use of the HemaSpot HF™ Blood Collection Device to Monitor Cortisol Chronobiology**
*Jeanette Hill - Spot On Sciences* (jeanetterhill@spotonsciences.com)

- Cardiovascular diseases (CVD) are the number one cause of death globally, representing 30% of all deaths and the majority of events occur in the early morning. To examine circadian effects on CVD biomarkers, blood samples were collected at 8 time points within a 24 h period with the HemaSpot HF collection device that enables self-collection at home. Cortisol displayed a diurnal expression pattern in all five donors that was consistent over three separate days. Collection and analysis of blood samples at relevant time points over a 24 h time period will provide important data for circadian levels of key analytes for chronic disease.

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Wednesday 5:00 PM
Poster #63 in Exhibit Hall
**Analyte Stability from Dried Blood Collected on HemaSpot-HF™ Devices**
*James Hill - Spot On Sciences, Inc.* (jameshill@spotonsciences.com)

- Representative analytes including small molecules, proteins and nucleic acids, were examined for their long-term storage stability on HemaSpot-HF devices stored at various temperatures and humidities. Small molecules cortisol, nifedipine, and tolbutamide enzyme protein β-D-Galactosidase and nucleic acids micro RNA; miR155, messenger RNA; β-Actin and ribosomal RNA; 18S were followed over the course of 12 months while stored at temperatures from -20 °C to 45 °C. Shorter term stability trials at >95% humidity were also followed over 4 weeks from room temperature to 45 °C. Analysis of the small molecules was performed by LC-MS/MS as was analysis of the enzymatic activity of β-D-Gal, by monitoring the formation of 4-methylumbelliferone from 4-MU- β-D-galactose. Analysis of the nucleic acids was performed by qPCR.

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Wednesday 3:00 PM
Poster #64 in Exhibit Hall
**Automated Tumor Typing of Tissue Sections Based on MALDI Mass Spectrometry Imaging Data and Machine Learning Using Characteristic Spectral Patterns**
*Tobias Boskamp - University of Bremen* (tboskamp@uni-bremen.de)

- We present an automated classification method for MALDI mass spectrometry imaging data with applications to tumor typing of FFPE tissue sections. The proposed method consists of a) data pre-processing, b) identification of characteristic spectral patterns using non-negative matrix factorization (NMF), and c) applying linear discriminant analysis (LDA) for classification. We apply this method to the discrimination of breast, lung, colon and pancreas cancer. MALDI data has been acquired from eight tissue micro arrays (TMAs), two for each tumor type, with a total of 943 cores from 285 patients. Four TMAs have been used for training, the remaining four TMAs for validation. A sensitivity on core level of 100.0% (lung), 99.5% (pancreas), 100.0% (colon), and 100.0% (breast) was achieved. Only limited effects of different preprocessing variants (normalization, filtering) were observed.
Steroid Hormones in Serum, a Simply, Accurate, Sensitive and Not Extractable Kit Ready to Use by LC-MS/MS

Stefano Sartori - Eureka srl - Lab Division (sartori@eurekaone.com)

- Alifax - Eureka Steroid Hormones in serum kit ready to use permits the simultaneous analysis of the most important steroids in a un single chromatography sample run (17-OH-Progesterone, Dehydroepiandrosterone (DHEA), Dehydroepiandrosterone sulfate (DHEAS), Androstenedione, Cortisol, 11-Deoxycortisol, Corticosterone, Aldosterone, Testosterone, Dihydrotestosterone, Androsterone, Estrone, Estradiol, Pregnenolone, 17-OH-Pregnenolone, Progesterone, 11-Deoxycorticosterone) after a simple matrix deproteinisation. To analyze correctly full panel in routine it's necessary to have a medium/high level mass QQQ detector coupled with an UHPLC. Seven levels of serum calibrators and two levels of serum controls are available, covering clinical range concentration values.

Ultra-Fast Quantification of Antidepressants in Urine at 9 Seconds Per Sample Using LDTD-MS/MS

Alex Birsan - Phytronix Technologies (a.birsan@phytronix.com)

- According to a 2011 National Center for Health Statistics (NCHS) report, the rate of Antidepressants use in USA increased by almost 400% between 2005 and 2008 for people older than 12 years old. The federal government's health statisticians figure that about one in every 10 Americans takes at least one antidepressant. By their calculation, antidepressants were the third most common prescribed medication taken by Americans. These numbers are only likely to increase over the years. Using mass spectrometry combined with high-throughput LDTD ion source enhances specificity at equivalent or better speed for the quantification of 7 Antidepressants in human urine. Using only a basic liquid-liquid extraction for the sample preparation, we are able to achieve a robust method with precision and accuracy at a speed of 9 seconds per sample.

Integration of Steroids Analysis in Serum Using LC-MS/MS with Full-automated Sample Preparation

Brian Feild - Shimadzu Scientific Instruments (bjfeild@shimadzu.com)

- Currently sample preparation for the detection of steroids in serum by LC-MS/MS involves complex offline extraction methods such as solid phase extraction or liquid/liquid extraction, all of which require additional sample concentration and reconstitution in an appropriate solvent. These sample preparation methods are time-consuming, often taking 1 hour or more per sample, and are more vulnerable to variability due to errors in manual preparation. Our approach to offering a high sensitivity steroid detection method and timely, automated analysis of multiple samples is to use the automated sample preparation system coupled to the detection capabilities of a high-sensitivity LC-MS/MS.

High Throughput Analysis for Novel Oral Anticoagulants Using LC-MS/MS System Integrated with Automated Sample Preparation

Daisuke Kawakami - Shimadzu Corporation (daikawa@shimadzu.co.jp)

- LC-MS/MS has become essential tool for monitoring the concentration of drugs in biological samples due to its high level of sensitivity and specificity; however, manual sample preparation often involves several complicated manual steps which can introduce error into the results. In this study, we investigated the ability to analyze for Novel Oral Anticoagulants by LC-MS/MS using automated sample preparation to process large sample sets. We validated the automated method by comparing the data collected on the automated system to the data collected using a manual sample preparation protocol.
**High Throughput Quantitation for Therapeutic Drug Monitoring with Open Access LC/MS/MS System**

Miho Kawashima - Shimadzu Corporation (k-miho@shimadzu.co.jp)

- In this paper, we introduce four research use only LC/MS/MS methods for therapeutic drug monitoring (TDM), mycophenolic acid, sunitinib and axitinib, voriconazole, itraconazole, using a mobile phase switching system. With an open access user interface software (Open Solution QuantAnalytics, Shimadzu), analysts can start LC/MS/MS measurement quickly only by selecting a method and placing vials in the specified autosampler plate positions and review the data in office as soon as it becomes available on the designated data server. High-throughput LC/MS/MS methods for TDM with a new data acquisition and processing software was developed.

**Developed Method for Acylcarnitine Analysis in Serum Using LC-MS/MS as a Clinical Exam**

Hironori Kobayashi - Shimane University Faculty of Medicine (bakki@med.shimane-u.ac.jp)

- Method for determination of acylcarnitine by LC-MS/MS was developed to improve existing techniques that are not suitable for the clinical diagnosis tests due to quantitative differences between analytical instruments and the lack of internal calibrator. The validation of AC determination assay in serum was conducted and the intra- and inter-day repeatability, accuracy, linearity, recovery and precision were confirmed. The previously developed method was simplified and precision was significantly improved by addition of the calibrator. We believe that this method has the potential to become standard method for clinical exam of positively screened infants or follow-up patients.

**Applying a Proteoform Profiling Method for Neurological Disorder Biomarker Discovery**

Nicolai Bache - Bruker Daltonics, Inc. (nicolai.bache@bruker.com)

- In this study we have used a quantitative proteoform profiling experiment to detect and identify several potential biomarkers for Alzheimer’s disease based on cerebrospinal fluid (CSF). We were able to comfortably and reproducibly detect more than 1500 proteoforms in each sample leading to the detection and identification of 77 differentially regulated proteoforms (potential biomarker candidates) which are currently being identified and validated through a scheduled top-down MS/MS approach. Many of those correspond to proteoforms of proteins carrying a specific modification, a mutation or having undergone a proteolytic modification which would have made their characterization much more challenging, if not impossible, with a bottom-up workflow.

**Fast Analysis of Low pg/mL Level Testosterone in Serum by Bruker TQ LC/MS**

Zicheng Yang - Bruker Daltonics (zicheng.yang@bruker.com)

- Testosterone concentrations in adult females and children (male and female) are an order of magnitude lower than adult male testosterone concentrations and require a sensitive and specific analytical method to accurately determine the testosterone level. A sensitive method for the quantification of total testosterone in serum was developed using Bruker TQ LC/MS system. Excellent sensitivity, linearity and dynamic range were obtained with a LOD of 1 pg/mL, R2 > 0.99, and greater than four orders of dynamic range. The low pg/mL level detection with wide dynamic detection range will cover the clinical research needs.

**Comparison of Several Approaches for Vitamin D Metabolite Analysis**

Xuejun Zang - Orochem Technologies Inc (june@orochem.com)

- LC-MS/MS method has emerged as a reliable method of choice for vitamin D metabolite analysis. However, it’s easily affected by phospholipids content in the serum samples. We present two different vitamin D metabolites extraction methods. One is using Vitamin D extraction plate. The process is simple and high throughput. For 96-well plate, the process time is less than 10 minutes. Most matrix interferences are removed, while the recoveries of mono- and di-hydroxyl vitamin D are good. Another procedure is using polymeric SPE extraction product. The final recoveries of vitamin D metabolites are all above 86%.
The Novel LC-MS/MS System Integrated with Automated Sample Preparation for Drugs Analyses

Hikaru Shibata - Shimadzu Scientific Instruments Inc. (hishibata@shimadzu.com)

The limits of traditional analytical methods, such as LC-MS/MS, are progressively being pushed further with regard to robustness, ease of use, sensitivity, throughput, cost effectiveness and accuracy. Here we propose a novel approach to automated sample preparation by combining an on-line automated sample preparation instrument (CLAM-2000, Shimadzu) for LC-MS/MS analysis (LCMS-8040, Shimadzu). In this study, we investigated ability to analyze for antiepileptic drugs and antiarrhythmic drugs using the CLAM-2000 for automated sample preparation for LC-MS/MS. We validated feasibility of this system by measuring precision and accuracy of the drugs which have various chemical properties.

A Novel Drug Screening Protocol for Acidic, Basic, and Neutral in Hydrolyzed Urine Using Supported Liquid Extraction Prior to LC-MS/MS Analysis

Dan Menasco - Biotage (dan.menasco@biotage.com)

Introduction: Screening urine samples quickly for drugs is typically performed by immunoassay analyzers. Once sample test positive for drug presence then an additional step is needed to qualitatively and quantitatively confirm the identity and amount of drug identified from the initial screening. Ideally, the workflow of a laboratory could be optimized by conducting the screening and confirmation analysis via tandem LC-MS simultaneously. To accomplish this, a reliable sample preparation method is needed to extract acidic, basic and neutral drugs from urine. This poster will outline the details for a novel sample preparation method can be used to extract acidic, basic and neutral drugs from hydrolysed urine samples. Over 32 different drugs were extracted from urine samples quickly and analysed qualitatively and quantitatively.
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